

[illegible]

[illegible][illegible]

83	12.4	45.9	24	26	AAV63967	PCR primer used to	156	11.6	44.4	17	17	AAV13972	3 element construct
84	12.4	45.9	24	24	ABG03061	Oligonucleotide ad	157	11.6	44.4	27	22	AAV28482	Random oligonucleo
85	12.4	45.9	24	19	AAV44274	IFR A1 intracytop	158	11.6	44.4	27	24	AAV65046	Sanjour et al. 1993
86	12.4	45.9	25	13	AAV60676	HLA HLA A gene PCR	159	11.6	44.4	29	19	AAV76966	Preparation of cell
87	12.4	45.9	27	18	AAV75455	Primer MVL10 for k	160	11.6	44.4	30	19	AAV01249	Human protein in 1
88	12.4	45.9	29	21	AAV29474	Forward Gene Spec	161	11.6	44.4	30	22	AAV54836	Human protein in 1
89	12.4	45.9	30	19	AAV17108	PCR primer/forward	162	11.6	44.4	31	18	AAV64626	Stable bound stat
90	12.4	45.9	34	24	AAV15493	PCR primer 4 for c	163	11.6	44.4	31	18	AAV64541	Stable bound stat
91	12.4	45.9	17	17	AAV81136	Human c myb hamer	164	11.6	44.4	33	24	AAV87605	Human protein in 1
92	12.4	45.9	19	19	AAV97941	Human EGF p. target	165	11.6	44.4	34	22	AAV54835	Primer used in 1
93	12.4	45.9	19	19	AAV78415	Human rhinovirus 1	166	11.6	44.4	34	22	AAV54837	Human protein in 1
94	12.4	45.9	19	21	AAV21192	Canine T-cell rece	167	11.6	44.4	34	22	AAV54838	Human protein in 1
95	12.4	45.9	19	21	AAV22265	Canine T-cell rece	168	11.6	44.4	35	24	AAV73116	Human protein in 1
96	12.4	45.9	19	22	AAV17943	PCR primer for a m	169	11.6	44.4	35	24	AAV18497	Human protein in 1
97	12.4	45.9	19	24	AAV17944	Human cytomeg 1	170	11.6	44.4	35	24	AAV18497	Human protein in 1
98	12.4	45.9	24	21	AAV1467	PCR primer Y137 us	171	11.6	44.4	35	24	AAV18497	Human protein in 1
99	12.4	45.9	25	18	AAV9798	Human and mouse	172	11.6	44.4	35	24	AAV18497	Human protein in 1
100	12.4	45.9	25	21	AAV9800	16S rRNA gene p.p	173	11.6	44.4	35	24	AAV18497	Human protein in 1
101	12.4	45.9	25	21	AAV9495	HLA DQB1 gene PCR	174	11.6	44.4	35	24	AAV18497	Human protein in 1
102	12.4	45.9	25	24	AAV14122	Human GEMT1 25m	175	11.6	44.4	35	24	AAV18497	Human protein in 1
103	12.4	45.9	26	26	AAV68435	Canine factor VII	176	11.6	44.4	35	24	AAV18497	Human protein in 1
104	12.4	45.9	26	21	AAV1467	Canine factor VII	177	11.6	44.4	35	24	AAV18497	Human protein in 1
105	12.4	45.9	28	21	AAV1467	Canine factor VII	178	11.6	44.4	35	24	AAV18497	Human protein in 1
106	12.4	45.9	28	19	AAV9445	Streptococcus sps	179	11.6	44.4	35	24	AAV18497	Human protein in 1
107	12.4	45.9	28	19	AAV9445	Streptococcus sps	180	11.6	44.4	35	24	AAV18497	Human protein in 1
108	12.4	45.9	28	19	AAV9445	Streptococcus sps	181	11.6	44.4	35	24	AAV18497	Human protein in 1
109	12.4	45.9	28	19	AAV9445	Streptococcus sps	182	11.6	44.4	35	24	AAV18497	Human protein in 1
110	12.4	45.9	28	19	AAV9445	Streptococcus sps	183	11.6	44.4	35	24	AAV18497	Human protein in 1
111	12.4	45.9	28	19	AAV9445	Streptococcus sps	184	11.6	44.4	35	24	AAV18497	Human protein in 1
112	12.4	45.9	28	19	AAV9445	Streptococcus sps	185	11.6	44.4	35	24	AAV18497	Human protein in 1
113	12.4	45.9	28	19	AAV9445	Streptococcus sps	186	11.6	44.4	35	24	AAV18497	Human protein in 1
114	12.4	45.9	28	19	AAV9445	Streptococcus sps	187	11.6	44.4	35	24	AAV18497	Human protein in 1
115	12.4	45.9	28	19	AAV9445	Streptococcus sps	188	11.6	44.4	35	24	AAV18497	Human protein in 1
116	12.4	45.9	28	19	AAV9445	Streptococcus sps	189	11.6	44.4	35	24	AAV18497	Human protein in 1
117	12.4	45.9	28	19	AAV9445	Streptococcus sps	190	11.6	44.4	35	24	AAV18497	Human protein in 1
118	12.4	45.9	28	19	AAV9445	Streptococcus sps	191	11.6	44.4	35	24	AAV18497	Human protein in 1
119	12.4	45.9	28	19	AAV9445	Streptococcus sps	192	11.6	44.4	35	24	AAV18497	Human protein in 1
120	12.4	45.9	28	19	AAV9445	Streptococcus sps	193	11.6	44.4	35	24	AAV18497	Human protein in 1
121	12.4	45.9	28	19	AAV9445	Streptococcus sps	194	11.6	44.4	35	24	AAV18497	Human protein in 1
122	12.4	45.9	28	19	AAV9445	Streptococcus sps	195	11.6	44.4	35	24	AAV18497	Human protein in 1
123	12.4	45.9	28	19	AAV9445	Streptococcus sps	196	11.6	44.4	35	24	AAV18497	Human protein in 1
124	12.4	45.9	28	19	AAV9445	Streptococcus sps	197	11.6	44.4	35	24	AAV18497	Human protein in 1
125	12.4	45.9	28	19	AAV9445	Streptococcus sps	198	11.6	44.4	35	24	AAV18497	Human protein in 1
126	12.4	45.9	28	19	AAV9445	Streptococcus sps	199	11.6	44.4	35	24	AAV18497	Human protein in 1
127	12.4	45.9	28	19	AAV9445	Streptococcus sps	200	11.6	44.4	35	24	AAV18497	Human protein in 1
128	12.4	45.9	28	19	AAV9445	Streptococcus sps	201	11.6	44.4	35	24	AAV18497	Human protein in 1
129	12.4	45.9	28	19	AAV9445	Streptococcus sps	202	11.6	44.4	35	24	AAV18497	Human protein in 1
130	12.4	45.9	28	19	AAV9445	Streptococcus sps	203	11.6	44.4	35	24	AAV18497	Human protein in 1
131	12.4	45.9	28	19	AAV9445	Streptococcus sps	204	11.6	44.4	35	24	AAV18497	Human protein in 1
132	12.4	45.9	28	19	AAV9445	Streptococcus sps	205	11.6	44.4	35	24	AAV18497	Human protein in 1
133	12.4	45.9	28	19	AAV9445	Streptococcus sps	206	11.6	44.4	35	24	AAV18497	Human protein in 1
134	12.4	45.9	28	19	AAV9445	Streptococcus sps	207	11.6	44.4	35	24	AAV18497	Human protein in 1
135	12.4	45.9	28	19	AAV9445	Streptococcus sps	208	11.6	44.4	35	24	AAV18497	Human protein in 1
136	12.4	45.9	28	19	AAV9445	Streptococcus sps	209	11.6	44.4	35	24	AAV18497	Human protein in 1
137	12.4	45.9	28	19	AAV9445	Streptococcus sps	210	11.6	44.4	35	24	AAV18497	Human protein in 1
138	12.4	45.9	28	19	AAV9445	Streptococcus sps	211	11.6	44.4	35	24	AAV18497	Human protein in 1
139	12.4	45.9	28	19	AAV9445	Streptococcus sps	212	11.6	44.4	35	24	AAV18497	Human protein in 1
140	12.4	45.9	28	19	AAV9445	Streptococcus sps	213	11.6	44.4	35	24	AAV18497	Human protein in 1
141	12.4	45.9	28	19	AAV9445	Streptococcus sps	214	11.6	44.4	35	24	AAV18497	Human protein in 1
142	12.4	45.9	28	19	AAV9445	Streptococcus sps	215	11.6	44.4	35	24	AAV18497	Human protein in 1
143	12.4	45.9	28	19	AAV9445	Streptococcus sps	216	11.6	44.4	35	24	AAV18497	Human protein in 1
144	12.4	45.9	28	19	AAV9445	Streptococcus sps	217	11.6	44.4	35	24	AAV18497	Human protein in 1
145	12.4	45.9	28	19	AAV9445	Streptococcus sps	218	11.6	44.4	35	24	AAV18497	Human protein in 1
146	12.4	45.9	28	19	AAV9445	Streptococcus sps	219	11.6	44.4	35	24	AAV18497	Human protein in 1
147	12.4	45.9	28	19	AAV9445	Streptococcus sps	220	11.6	44.4	35	24	AAV18497	Human protein in 1
148	12.4	45.9	28	19	AAV9445	Streptococcus sps	221	11.6	44.4	35	24	AAV18497	Human protein in 1
149	12.4	45.9	28	19	AAV9445	Streptococcus sps	222	11.6	44.4	35	24	AAV18497	Human protein in 1
150	12.4	45.9	28	19	AAV9445	Streptococcus sps	223	11.6	44.4	35	24	AAV18497	Human protein in 1
151	12.4	45.9	28	19	AAV9445	Streptococcus sps	224	11.6	44.4	35	24	AAV18497	Human protein in 1
152	12.4	45.9	28	19	AAV9445	Streptococcus sps	225	11.6	44.4	35	24	AAV18497	Human protein in 1
153	12.4	45.9	28	19	AAV9445	Streptococcus sps	226	11.6	44.4	35	24	AAV18497	Human protein in 1
154	12.4	45.9	28	19	AAV9445	Streptococcus sps	227	11.6	44.4	35	24	AAV18497	Human protein in 1
155	12.4	45.9	28	19	AAV9445	Streptococcus sps	228	11.6	44.4	35	24	AAV18497	Human protein in 1
156	12.4	45.9	28	19	AAV9445	Streptococcus sps	229	11.6	44.4	35	24	AAV18497	Human protein in 1

Downloaded from <http://ajph.org/> on November 10, 2014

10	14	51.9	27	15	AA068664	Protein to activate
11	14	51.9	27	16	AA061544	Micrococcus gale
12	14	51.9	27	17	AA051245	Protein to activate
13	13.8	51.1	32	20	AA033623	Protein used for
14	13.6	50.4	24	22	AA065664	Protein to activate
15	13.6	50.4	27	15	AA077401	Human cell virus
16	13.6	50.4	33	15	AA077329	Human cell virus
17	12.4	48.6	23	23	AA067145	Human cell virus
18	13.4	48.6	23	23	AA067145	Human cell virus
19	13.2	48.9	18	24	AA010655	Human cell virus
20	13.2	48.9	20	19	AA013842	Human cell virus
21	13.2	48.9	22	10	AA016944	Human cell virus
22	13.2	48.9	26	19	AA075561	Human cell virus
23	13.2	48.9	26	19	AA075562	Human cell virus
24	13.2	48.9	27	17	AA070662	Human cell virus
25	13.2	48.9	28	17	AA013103	Human cell virus
26	13.2	48.9	32	13	AA075562	Human cell virus
27	13.2	48.9	32	13	AA075562	Human cell virus
28	13.2	48.9	32	13	AA075562	Human cell virus
29	13.2	48.9	32	13	AA075562	Human cell virus
30	13.2	48.9	32	13	AA075562	Human cell virus
31	13.2	48.9	32	13	AA075562	Human cell virus
32	13.2	48.9	32	13	AA075562	Human cell virus
33	13.2	48.9	32	13	AA075562	Human cell virus
34	13.2	48.9	32	13	AA075562	Human cell virus
35	13.2	48.9	32	13	AA075562	Human cell virus
36	13.2	48.9	32	13	AA075562	Human cell virus
37	13.2	48.9	32	13	AA075562	Human cell virus
38	13.2	48.9	32	13	AA075562	Human cell virus
39	13.2	48.9	32	13	AA075562	Human cell virus
40	13.2	48.9	32	13	AA075562	Human cell virus
41	13.2	48.9	32	13	AA075562	Human cell virus
42	13.2	48.9	32	13	AA075562	Human cell virus
43	13.2	48.9	32	13	AA075562	Human cell virus
44	13.2	48.9	32	13	AA075562	Human cell virus
45	13.2	48.9	32	13	AA075562	Human cell virus
46	13.2	48.9	32	13	AA075562	Human cell virus
47	13.2	48.9	32	13	AA075562	Human cell virus
48	13.2	48.9	32	13	AA075562	Human cell virus
49	13.2	48.9	32	13	AA075562	Human cell virus
50	13.2	48.9	32	13	AA075562	Human cell virus
51	13.2	48.9	32	13	AA075562	Human cell virus
52	13.2	48.9	32	13	AA075562	Human cell virus
53	13.2	48.9	32	13	AA075562	Human cell virus
54	13.2	48.9	32	13	AA075562	Human cell virus
55	13.2	48.9	32	13	AA075562	Human cell virus
56	13.2	48.9	32	13	AA075562	Human cell virus
57	13.2	48.9	32	13	AA075562	Human cell virus
58	13.2	48.9	32	13	AA075562	Human cell virus
59	13.2	48.9	32	13	AA075562	Human cell virus
60	13.2	48.9	32	13	AA075562	Human cell virus
61	13.2	48.9	32	13	AA075562	Human cell virus
62	13.2	48.9	32	13	AA075562	Human cell virus
63	13.2	48.9	32	13	AA075562	Human cell virus
64	13.2	48.9	32	13	AA075562	Human cell virus
65	13.2	48.9	32	13	AA075562	Human cell virus
66	13.2	48.9	32	13	AA075562	Human cell virus
67	13.2	48.9	32	13	AA075562	Human cell virus
68	13.2	48.9	32	13	AA075562	Human cell virus
69	13.2	48.9	32	13	AA075562	Human cell virus
70	13.2	48.9	32	13	AA075562	Human cell virus
71	13.2	48.9	32	13	AA075562	Human cell virus
72	13.2	48.9	32	13	AA075562	Human cell virus
73	13.2	48.9	32	13	AA075562	Human cell virus



REFERENCE AP16720.1 21-07-04-99
 KEYWORDS Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 19)
 TITLE beta-casein expressing constructs
 JOURNAL Patent: US 6287945-A 16-11-SEP-2001;
 FEATURES
 SOURCE 1..19
 /organism="unknown"
 BASE COUNT 3 a 4 c 6 g 6 t
 ORIGIN
 Query Match 47.4%; Score 12.8; DB 6; Length 19;
 Best Local Similarity 97.5%; Pred. No. 5.6e+05;
 Matches 14, Conservative 0, Mismatched 2, Indels 0, Gaps 0,
 3 CTGAGCAATACCTAAC 18
 16 CTGAGCAATACCTAAC 1

RESULT 31
 AR030433/c
 LOCUS AR030433 20 bp. DNA linear. PAT 20-SEP-1999
 DEFINITION Sequence 6 from patent US 5861273.
 ACCESSION AR030433
 VERSION AR030433.1 GI:5943647
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Olson,P.S. and Mascarenhas,D.
 TITLE Chromosomal expression of heterologous genes in bacterial cells
 JOURNAL Patent: US 5861273-A 6-19-JAN-1999;
 FEATURES
 SOURCE 1..20

Query Match 47.4%; Score 12.8; DB 6; Length 19;
 Best Local Similarity 97.5%; Pred. No. 5.6e+05;
 Matches 14, Conservative 0, Mismatched 2, Indels 0, Gaps 0,
 3 CTGAGCAATACCTAAC 18
 16 CTGAGCAATACCTAAC 1

RESULT 32
 AR030447/c
 LOCUS AR030447 20 bp. DNA linear. PAT 20-SEP-1999
 DEFINITION Sequence 20 from patent US 5861273.
 ACCESSION AR030447
 VERSION AR030447.1 GI:5943661
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Olson,P.S. and Mascarenhas,D.
 TITLE Chromosomal expression of heterologous genes in bacterial cells
 JOURNAL Patent: US 5861273-A 6-19-JAN-1999;
 FEATURES
 SOURCE 1..20
 /organism="unknown"
 BASE COUNT 3 a 4 c 6 g 7 t
 ORIGIN
 Query Match 47.4%; Score 12.8; DB 6; Length 20;
 Best Local Similarity 97.5%; Pred. No. 5.6e+05;
 Matches 14, Conservative 0, Mismatched 2, Indels 0, Gaps 0,
 3 CTGAGCAATACCTAAC 18
 17 CTGAGCAATACCTAAC 2

RESULT 33
 AR030490/c
 LOCUS AR030490 20 bp. DNA linear. PAT 20-SEP-1999
 DEFINITION Sequence 63 from patent US 5861273.
 ACCESSION AR030490
 VERSION AR030490.1 GI:5943704
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Olson,P.S. and Mascarenhas,D.
 TITLE Chromosomal expression of heterologous genes in bacterial cells
 JOURNAL Patent: US 5861273-A 6-19-JAN-1999;
 FEATURES
 SOURCE 1..20
 /organism="unknown"
 BASE COUNT 3 a 4 c 6 g 7 t
 ORIGIN
 Query Match 47.4%; Score 12.8; DB 6; Length 20;
 Best Local Similarity 97.5%; Pred. No. 5.6e+05;
 Matches 14, Conservative 0, Mismatched 2, Indels 0, Gaps 0,
 3 CTGAGCAATACCTAAC 18
 17 CTGAGCAATACCTAAC 2

RESULT 34
 AR030490/c
 LOCUS AR030490 20 bp. DNA linear. PAT 20-SEP-1999
 DEFINITION Sequence 63 from patent US 5861273.
 ACCESSION AR030490
 VERSION AR030490.1 GI:5943704
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Olson,P.S. and Mascarenhas,D.
 TITLE Chromosomal expression of heterologous genes in bacterial cells
 JOURNAL Patent: US 5861273-A 6-19-JAN-1999;
 FEATURES
 SOURCE 1..20
 /organism="unknown"
 BASE COUNT 3 a 4 c 6 g 7 t
 ORIGIN
 Query Match 47.4%; Score 12.8; DB 6; Length 20;
 Best Local Similarity 97.5%; Pred. No. 5.6e+05;
 Matches 14, Conservative 0, Mismatched 2, Indels 0, Gaps 0,
 3 CTGAGCAATACCTAAC 18
 17 CTGAGCAATACCTAAC 2

SOURCE 1.33
/organism="synthetic construct"
/db xref="taxon:32436"
/note "Polythetic Nucleic Acid"

BASE COUNT 10 a 9 c 6 g 7 t
ORIGIN

Query Match 48.9% Score 13.2; DB 6; Length 31;
Best Local Similarity 69.2% Pred. No. 3.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCAATCAATCAATCAAT 30
||||| ||||| ||||| |||||
4 TCTTCAATCAATCAATCAAT 29

RESULT 25
ARI26247
LOCUS ARI26247
DEFINITION Sequence 9 from patent US 6190111
ACCESSION ARI26247
VERSION ARI26247.1 GI:14112840
KEYWORDS
SOURCE Unknown
ORGANISM Unknown
FEATURES
REFERENCE 1 (bases 1 to 35)
AUTHORS Stein,D.C. and Stover,C.K.
TITLE Vaccine delivery system
JOURNAL Patent: US 6180111-A 9 30 JAN-2001;
FEATURES
source 1.35
/organism="unknown"

BASE COUNT 16 a 3 c 6 g 10 t
ORIGIN

Query Match 48.9% Score 13.2; DB 6; Length 35;
Best Local Similarity 83.8% Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AATATCAATCAATCAAT 26
||||| ||||| ||||| |||||
12 AATATCAATCAATCAAT 25

RESULT 26
AX197112/c
LOCUS AX197112
DEFINITION Sequence 919 from Patent WO0151627.
ACCESSION AX197112
VERSION AX197112.1 GI:15387112
KEYWORDS
SOURCE Unknown
ORGANISM Unknown
FEATURES
REFERENCE 1 (bases 1 to 25)
AUTHORS Hupp,P.M., Wang,M.L., Parsons,J.D. and Faller,L.L.
TITLE Human A194 monoclonal antibodies and other monoclonal antibodies with myxoma
CYST nematode resistance
JOURNAL Patent: WO 0151627-A 819 19 JUL-2001;
FEATURES
source 1.25
/organism="Glycine max"
/db xref="taxon:3847"

BASE COUNT 4 a 3 c 9 g 10 t
ORIGIN

Query Match 48.1% Score 13; DB 6; Length 25;
Best Local Similarity 76.0% Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CTGACCAATCAATCAATCA 23
||||| ||||| ||||| |||||
25 CTGACCAATCAATCAATCA 5

RESULT 27
ARI91268
LOCUS ARI91268
DEFINITION Sequence 6756 from patent US 634639A.
ACCESSION ARI91268
VERSION ARI91268.1 GI:20237233
KEYWORDS
SOURCE Unknown
ORGANISM Unknown
FEATURES
REFERENCE 1 (bases 1 to 27)
AUTHORS Pavlov,P., Mesnygenov,I., Strohacker,D. and Fendler,H.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: EP 1494900 A 1767 17-SEP-2002;
FEATURES
source 1.27
/organism="unknown"

BASE COUNT 10 a 5 c 5 g 4 t
ORIGIN

Query Match 48.1% Score 13; DB 6; Length 27;
Best Local Similarity 72.0% Pred. No. 4.4e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 AGCAATCAATCAATCAAT 27
||||| ||||| ||||| |||||
1 AGCAATCAATCAATCAATCA 22

RESULT 28
ARI26504/c
LOCUS ARI26504
DEFINITION Sequence 131 from patent US 6180341.
ACCESSION ARI26504
VERSION ARI26504.1 GI:14113097
KEYWORDS
SOURCE Unknown
ORGANISM Unknown
FEATURES
REFERENCE 1 (bases 1 to 19)
AUTHORS Johnson,P.L., Scroggins,G. and Burke,E.A.
TITLE In vitro scanning saturation mutagenesis of proteins
JOURNAL Patent: US 6180341-A 131 30 JAN-2001;
FEATURES
source 1.19
/organism="unknown"

BASE COUNT 3 a 4 c 6 g 4 t
ORIGIN

Query Match 47.4% Score 12.9; DB 6; Length 19;
Best Local Similarity 87.5% Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CTGACCAATCAATCAAT 16
||||| ||||| ||||| |||||
16 CTGACCAATCAATCAAT 1

RESULT 29
ARI68720/c
LOCUS ARI68720
DEFINITION Sequence 16 from patent US 6287866.
ACCESSION ARI68720

AUTHORS Placzek, G
 TITLE Mice and mouse for fighting and identifying biological information
 JOURNAL Patent: US 5866163-A, 14-02-FEB-1999
 FEATURES Location/Qualifiers
 source 1..21
 BASE COUNT 10 a 6 c 0 g 5 t
 ORIGIN
 Query Match 48 48 Score 13.27 E-01 Length 21
 Best Local Similarity 83 83 Prod No 37405
 Matches 15 Conservative 0 Mismatches 3 Indels 0 Gaps 0
 QY 8 CATACCTAACGACAA 25
 4 CTATACCTAACGACAA 21
 DB
 RESULT 17
 ARI87925 ARI87925 27 bp DNA 1100bp PAT 00-APR-0000
 LOCATION 1..27
 DEFINITION Mice and mouse for fighting and identifying biological information
 VERSION ARI87925
 KEYWORDS ARI87925.1 GI:20233890
 SOURCE UNKNOWN
 ORGANISM Unclassified
 REFERENCE 1 (bases 1 to 27)
 AUTHORS PLYNN, P., MORGAN, J., STINCHFIELD, J. and PEEBODD, J
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 FEATURES Location/Qualifiers
 source 1..27
 BASE COUNT 3 a 10 c 10 g 1 t 10
 ORIGIN
 Query Match 48 48 Score 13.27 E-01 Length 27
 Best Local Similarity 83 83 Prod No 37405
 Matches 15 Conservative 0 Mismatches 3 Indels 0 Gaps 0
 QY 8 CATACCTAACGACAA 25
 4 CTATACCTAACGACAA 21
 DB
 RESULT 18
 ARI87925 ARI87925 27 bp DNA 1100bp PAT 00-APR-0000
 LOCATION 1..27
 DEFINITION Mice and mouse for fighting and identifying biological information
 VERSION ARI87925
 KEYWORDS ARI87925.1 GI:20233890
 SOURCE UNKNOWN
 ORGANISM Unclassified
 REFERENCE 1 (bases 1 to 27)
 AUTHORS PLYNN, P., MORGAN, J., STINCHFIELD, J. and PEEBODD, J
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 FEATURES Location/Qualifiers
 source 1..27
 BASE COUNT 3 a 10 c 10 g 1 t 10
 ORIGIN

QY 2 CCGACGATACCTAACGACAA 27
 26 CCGACGATACCTAACGACAA 1
 DB
 RESULT 19
 ARI87925 ARI87925 27 bp DNA 1100bp PAT 00-APR-0000
 LOCATION 1..27
 DEFINITION Mice and mouse for fighting and identifying biological information
 VERSION ARI87925
 KEYWORDS ARI87925.1 GI:20233890
 SOURCE UNKNOWN
 ORGANISM Unclassified
 REFERENCE 1 (bases 1 to 27)
 AUTHORS PLYNN, P., MORGAN, J., STINCHFIELD, J. and PEEBODD, J
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 FEATURES Location/Qualifiers
 source 1..27
 BASE COUNT 3 a 10 c 10 g 1 t 10
 ORIGIN
 QY 2 CCGACGATACCTAACGACAA 27
 26 CCGACGATACCTAACGACAA 1
 DB
 RESULT 20
 ARI87925 ARI87925 27 bp DNA 1100bp PAT 00-APR-0000
 LOCATION 1..27
 DEFINITION Mice and mouse for fighting and identifying biological information
 VERSION ARI87925
 KEYWORDS ARI87925.1 GI:20233890
 SOURCE UNKNOWN
 ORGANISM Unclassified
 REFERENCE 1 (bases 1 to 27)
 AUTHORS PLYNN, P., MORGAN, J., STINCHFIELD, J. and PEEBODD, J
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 FEATURES Location/Qualifiers
 source 1..27
 BASE COUNT 3 a 10 c 10 g 1 t 10
 ORIGIN

[illegible]

source 1..24
 /db_xref="taxon:5476"
 ORIGIN 1 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

Query Match 51.9% Score 14 DP 6 Length 24
 Best Local Similarity 77.3% Freq No. 1.6e-05
 Matches 17: Conservative 0 Mismatches 5 Indels 0 Gaps 0

CY 1 CTGACCATACCTAACGACCA 24
 DB 22 CTGACCATACCTAACGACCA 1

RESULT 8
 AX487214/c
 LOCUS 4814 bp from Patent WO200202251
 DEFINITION AX487214
 VERSION AX487214 1 01-02-2002
 KEYWORDS
 SOURCE Candida albicans
 ORGANISM Candida albicans
 Eukaryota, Fungi, Ascomycota, Saccharomycetes, Basidiomycota, Microsporidia, Saccharomycetales, Candida

REFERENCE 1
 Kasper, T., Kasper, F., Kasper, J., Kasper, H. and Kasper, K. L.
 TITLE Gene disruption methodologies for drug target discovery
 JOURNAL Patent: WO200202251 A 4814 11-01-2002
 Elitra Pharmaceuticals, Inc. (US)
 FEATURES 1..27
 location/Qualifiers
 /db_xref="taxon:5476"
 ORIGIN 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

BASE COUNT 6 a 5 c 5 g 11 t

ORIGIN 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

Query Match 51.9% Score 14 DP 6 Length 24
 Best Local Similarity 77.3% Freq No. 1.6e-05
 Matches 17: Conservative 0 Mismatches 5 Indels 0 Gaps 0

CY 5 GACCATACCTAACGACCAAT 26
 DB 25 GACCATACCTAACGACCAAT 4

RESULT 9
 AX259849
 LOCUS 26 bp from Patent WO200202251
 DEFINITION AX259849
 VERSION AX259849 1 01-02-2002
 KEYWORDS
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota, Metazoa, Chordata, Mammalia, Primates, Hominidae, Hominidae, Homo

REFERENCE 1
 Hugot, J. P., Thomas, G., Zouali, M., Lesage, S. and Chamailard, M.
 TITLE Genes involved in Crohn's disease: a study of 1000 patients
 JOURNAL Patients: WO 0172802 A 76 04 OCT 2001
 Fondation Jean Dausset-Cepi (Fr)

FEATURES 1..24
 location/Qualifiers
 /organism="Homo sapiens"
 ORIGIN 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

BASE COUNT 5 a 7 c 8 g 4 t

ORIGIN 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

Query Match 50.4% Score 13 DP 6 Length 24
 Best Local Similarity 80.0% Freq No. 2.4e-05
 Matches 16: Conservative 0 Mismatches 4 Indels 0 Gaps 0

source 1..24
 /db_xref="taxon:5476"
 ORIGIN 1 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

Query Match 51.9% Score 14 DP 6 Length 24
 Best Local Similarity 77.3% Freq No. 1.6e-05
 Matches 17: Conservative 0 Mismatches 5 Indels 0 Gaps 0

CY 1 CTGACCATACCTAACGACCA 24
 DB 22 CTGACCATACCTAACGACCA 1

RESULT 10
 AP184683
 LOCUS 27 bp from Patent US 6346398
 DEFINITION AP184683
 VERSION AP184683 1 01-02-2002
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 Eukaryota, Metazoa, Chordata, Mammalia, Primates, Hominidae, Hominidae, Homo

REFERENCE 1
 Kasper, T., Kasper, F., Kasper, J., Kasper, H. and Kasper, K. L.
 TITLE Gene disruption methodologies for drug target discovery
 JOURNAL Patent: US 6346398 A 171 12-FEB-2002
 Elitra Pharmaceuticals, Inc. (US)
 FEATURES 1..27
 location/Qualifiers
 /organism="unknown"
 ORIGIN 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

BASE COUNT 6 a 5 c 5 g 11 t

ORIGIN 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

Query Match 50.4% Score 13 DP 6 Length 24
 Best Local Similarity 80.0% Freq No. 2.4e-05
 Matches 16: Conservative 0 Mismatches 4 Indels 0 Gaps 0

CY 5 GACCATACCTAACGACCAAT 26
 DB 1 AGCGATACCTAACGACCAAT 21

RESULT 11
 AR045229/c
 LOCUS 33 bp from Patent US 646694
 DEFINITION AR045229
 VERSION AR045229 1 01-02-2002
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 Eukaryota, Metazoa, Chordata, Mammalia, Primates, Hominidae, Hominidae, Homo

REFERENCE 1
 Kasper, T., Kasper, F., Kasper, J., Kasper, H. and Kasper, K. L.
 TITLE Gene disruption methodologies for drug target discovery
 JOURNAL Patent: US 646694 A 171 12-FEB-2002
 Elitra Pharmaceuticals, Inc. (US)
 FEATURES 1..33
 location/Qualifiers
 /organism="unknown"
 ORIGIN 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33

BASE COUNT 5 a 9 c 8 g 11 t

ORIGIN 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33

Query Match 50.4% Score 13 DP 6 Length 24
 Best Local Similarity 80.0% Freq No. 2.4e-05
 Matches 16: Conservative 0 Mismatches 4 Indels 0 Gaps 0

CY 2 CTGACCATACCTAACGACCA 21
 DB 22 CTGACCATACCTAACGACCA 3

RESULT 12
 152281/c
 LOCUS 33 bp from Patent US 646694
 DEFINITION 152281
 VERSION 152281 1 01-02-2002
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 Eukaryota, Metazoa, Chordata, Mammalia, Primates, Hominidae, Hominidae, Homo

PD 04-DEC-1996
 PF 31-MAY-1995 JP 10-SEP-1994
 PI TSUCHIDA, NAOKO, MINEMASA YAMASHITA, TAMAKOCHI SAWASHI, HI
 YAMAMOTO, AKIHITO,
 PI MAHATA, HIDEHIRO, NAITO, TAKAHITO,
 PC CLONING AND CHARACTERIZATION OF A HUMAN CD45-RELATED GENE,
 CC strandness: Double,
 CC length: 351 bp,
 CC hybridization: No,
 CC anti-sense: No,
 FH Key,
 FH Location/Qualifiers
 FT promoter
 1..34.
 1..35
 /organism="Synthetic Construct"
 /db_xref="taxon:32630"
 13 a 5 c 8 g 9 t

BASE COUNT
 13 a 5 c 8 g 9 t

Query Match
 Best Local Similarity: 75.0%; Score 14.4; DB 6; Length 35;
 Matches 12, Conservative 0, Mismatches 4, Indels 0, Gaps 0.

RESULT 4
 LOCUS AX009821
 DEFINITION Sequence 7647 from Patent WO019846.
 ACCESSION AX009821
 VERSION AX009821.1 GI:1000976
 KEYWORDS
 SOURCE synthetic construct,
 ORGANISM synthetic construct,
 artificial sequences.
 REFERENCE
 1 Barany, F., Barany, M., Gervy, N.P., Fawcett, R. and Pflanz, P.
 Method of designing addressable array for determination of multiple amino
 acid sequences using oligonucleotide probes.
 JOURNAL JOURNAL OF MOLECULAR BIOLOGY 314:1-12 (1997)
 FEATURES
 source
 1..24
 /organism="Synthetic Construct"
 /db_xref="taxon:32630"
 /note="Hybridized to the probe"
 2 a 6 c 7 g 9 t

BASE COUNT
 2 a 6 c 7 g 9 t

Query Match
 Best Local Similarity: 94.0%; Score 14.4; DB 6; Length 35;
 Matches 16, Conservative 0, Mismatches 3, Indels 0, Gaps 0.

RESULT 5
 LOCUS AX081643
 DEFINITION Sequence 148 from Patent WO019846.
 ACCESSION AX081643
 VERSION AX081643.1 GI:13170468
 KEYWORDS
 SOURCE synthetic construct,
 ORGANISM synthetic construct,
 artificial sequences.
 REFERENCE
 1 (bases 1 to 33)

AUTHORS
 Berthel, P., Dalemans, W.G., Demmel, P., Desguere, J.S., Fawcett, R.,
 Leber, A.S., Poolman, J.S., Thilly, G.S., Thoma, J.S. and Voelt, P.G.
 TITLE
 Genetically engineered blood vaccine
 JOURNAL
 VACCINE 19:1489-1496 (2001)
 REFERENCE
 Berthel, P., Dalemans, W.G., Demmel, P., Desguere, J.S., Fawcett, R.,
 Leber, A.S., Poolman, J.S., Thilly, G.S., Thoma, J.S. and Voelt, P.G.
 Genetically engineered blood vaccine
 VACCINE 19:1489-1496 (2001)
 FEATURES
 source
 1..33
 /organism="Synthetic Construct"
 /db_xref="taxon:32630"
 /note="Direct 5' X primer"
 14 a 9 c 5 g 5 t

BASE COUNT
 14 a 9 c 5 g 5 t

Query Match
 Best Local Similarity: 70.4%; Score 14.4; DB 6; Length 33;
 Matches 12, Conservative 0, Mismatches 8, Indels 0, Gaps 0.

RESULT 6
 LOCUS AX374824
 DEFINITION Sequence 148 from Patent WO0209746.
 ACCESSION AX374824
 VERSION AX374824.1 GI:1103726
 KEYWORDS
 SOURCE synthetic construct,
 ORGANISM synthetic construct,
 artificial sequences.
 REFERENCE
 1 Berthel, P., Dalemans, W.G., Demmel, P., Desguere, J.S., Fawcett, R.,
 Leber, A.S., Poolman, J.S., Thilly, G.S., Thoma, J.S. and Voelt, P.G.
 Genetically engineered blood vaccine
 VACCINE 19:1489-1496 (2001)
 FEATURES
 source
 1..33
 /organism="Synthetic Construct"
 /db_xref="taxon:32630"
 /note="Direct 5' X primer"
 24 a 9 c 5 g 5 t

BASE COUNT
 24 a 9 c 5 g 5 t

Query Match
 Best Local Similarity: 94.0%; Score 14.4; DB 6; Length 33;
 Matches 12, Conservative 0, Mismatches 6, Indels 0, Gaps 0.

RESULT 7
 LOCUS AX488217
 DEFINITION Sequence 148 from Patent WO0209746.
 ACCESSION AX488217
 VERSION AX488217.1 GI:22222297
 KEYWORDS
 SOURCE synthetic construct,
 ORGANISM synthetic construct,
 artificial sequences.
 REFERENCE
 1 Berthel, P., Dalemans, W.G., Demmel, P., Desguere, J.S., Fawcett, R.,
 Leber, A.S., Poolman, J.S., Thilly, G.S., Thoma, J.S. and Voelt, P.G.
 Genetically engineered blood vaccine
 VACCINE 19:1489-1496 (2001)
 FEATURES
 source
 1..33
 /organism="Synthetic Construct"
 /db_xref="taxon:32630"
 /note="Direct 5' X primer"
 24 a 9 c 5 g 5 t

C 942	10	37.0	17	6	AP034147	AP034147 Sequence
C 943	10	37.0	17	6	AX059476	AX059476 Sequence
C 944	10	37.0	17	6	EP005941	EP005941 Cephalos
C 945	10	37.0	17	6	173129	173129 Sequence 2
C 946	10	37.0	18	6	AP049644	AP049644 Sequence
C 947	10	37.0	18	6	AP064552	AP064552 Sequence
C 948	10	37.0	18	6	AP140362	AP140362 Sequence
C 949	10	37.0	18	6	AP165417	AP165417 Sequence
C 950	10	37.0	18	6	AP160841	AP160841 Sequence
C 951	10	37.0	18	6	AP181657	AP181657 Sequence
C 952	10	37.0	18	6	SP0002174	SP0002174 Sequence
C 953	10	37.0	18	6	EP008988	EP008988 Spss pol
C 954	10	37.0	18	6	EP004261	EP004261 Novel ST
C 955	10	37.0	19	6	AA09212	AA09212 Sequence 2
C 956	10	37.0	19	6	AP000157	AP000157 Sequence
C 957	10	37.0	19	6	AP004722	AP004722 Sequence
C 958	10	37.0	19	6	AP059278	AP059278 Sequence
C 959	10	37.0	19	6	AX130048	AX130048 Sequence
C 960	10	37.0	19	6	AX130546	AX130546 Sequence
C 961	10	37.0	19	6	AX133921	AX133921 Sequence
C 962	10	37.0	19	6	AX133257	AX133257 Sequence
C 963	10	37.0	19	6	AX134254	AX134254 Sequence
C 964	10	37.0	19	6	AX352994	AX352994 Sequence
C 965	10	37.0	19	6	AX362839	AX362839 Sequence
C 966	10	37.0	19	6	134654	134654 Sequence 7
C 967	10	37.0	19	6	165452	165452 Sequence 8
C 968	10	37.0	20	6	EP007412	EP007412 Sequence
C 969	10	37.0	20	6	AA46543	AA46543 Sequence 2
C 970	10	37.0	20	6	AA46544	AA46544 Sequence 3
C 971	10	37.0	20	6	AA46545	AA46545 Sequence 4
C 972	10	37.0	20	6	AP031003	AP031003 Sequence
C 973	10	37.0	20	6	AP034935	AP034935 Sequence
C 974	10	37.0	20	6	AP1070703	AP1070703 Sequence
C 975	10	37.0	20	6	AP106945	AP106945 Sequence
C 976	10	37.0	20	6	AP139457	AP139457 Sequence
C 977	10	37.0	21	6	AP157717	AP157717 Sequence
C 978	10	37.0	20	6	AP178816	AP178816 Sequence
C 979	10	37.0	21	6	AP207737	AP207737 Sequence
C 980	10	37.0	21	6	AX131966	AX131966 Sequence
C 981	10	37.0	20	6	AX138976	AX138976 Sequence
C 982	10	37.0	20	6	AX2067528	AX2067528 Sequence
C 983	10	37.0	20	6	AX294558	AX294558 Sequence
C 984	10	37.0	20	6	AX295137	AX295137 Sequence
C 985	10	37.0	20	6	AX400954	AX400954 Sequence
C 986	10	37.0	20	6	AX348171	AX348171 Sequence
C 987	10	37.0	20	6	AX341895	AX341895 Sequence
C 988	10	37.0	20	6	EP02571	EP02571 Sequence
C 989	10	37.0	20	6	EP02571	EP02571 Sequence
C 990	10	37.0	20	6	170598	170598 Sequence 1
C 991	10	37.0	21	6	AP041200	AP041200 Sequence
C 992	10	37.0	21	6	AP041200	AP041200 Sequence
C 993	10	37.0	21	6	AP054704	AP054704 Sequence
C 994	10	37.0	21	6	AR054267	AR054267 Sequence
C 995	10	37.0	21	6	AR054469	AR054469 Sequence
C 996	10	37.0	21	6	AP116503	AP116503 Sequence
C 997	10	37.0	21	6	AP154090	AP154090 Sequence
C 998	10	37.0	21	6	AP154952	AP154952 Sequence
C 999	10	37.0	21	6	AP164544	AP164544 Sequence
C1000	10	37.0	21	6	AP182957	AP182957 Sequence

ALIGNMENTS

RESULT 1			
GENUS	AX032826	27 bp	linear
DEFINITION	AX032826.1 from <i>Leishmania</i>		
ACCESSION	AX032826		
VERSION	AX032826.1		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM			

REFERENCE	1 (bases 1 to 27)	2 (bases 1 to 27)	3 (bases 1 to 27)	4 (bases 1 to 27)	5 (bases 1 to 27)	6 (bases 1 to 27)	7 (bases 1 to 27)	8 (bases 1 to 27)	9 (bases 1 to 27)	10 (bases 1 to 27)	11 (bases 1 to 27)	12 (bases 1 to 27)	13 (bases 1 to 27)	14 (bases 1 to 27)	15 (bases 1 to 27)	16 (bases 1 to 27)	17 (bases 1 to 27)	18 (bases 1 to 27)	19 (bases 1 to 27)	20 (bases 1 to 27)	21 (bases 1 to 27)	22 (bases 1 to 27)	23 (bases 1 to 27)	24 (bases 1 to 27)	25 (bases 1 to 27)	26 (bases 1 to 27)	27 (bases 1 to 27)	28 (bases 1 to 27)	29 (bases 1 to 27)	30 (bases 1 to 27)	31 (bases 1 to 27)	32 (bases 1 to 27)	33 (bases 1 to 27)	34 (bases 1 to 27)	35 (bases 1 to 27)	36 (bases 1 to 27)	37 (bases 1 to 27)	38 (bases 1 to 27)	39 (bases 1 to 27)	40 (bases 1 to 27)	41 (bases 1 to 27)	42 (bases 1 to 27)	43 (bases 1 to 27)	44 (bases 1 to 27)	45 (bases 1 to 27)	46 (bases 1 to 27)	47 (bases 1 to 27)	48 (bases 1 to 27)	49 (bases 1 to 27)	50 (bases 1 to 27)	51 (bases 1 to 27)	52 (bases 1 to 27)	53 (bases 1 to 27)	54 (bases 1 to 27)	55 (bases 1 to 27)	56 (bases 1 to 27)	57 (bases 1 to 27)	58 (bases 1 to 27)	59 (bases 1 to 27)	60 (bases 1 to 27)	61 (bases 1 to 27)	62 (bases 1 to 27)	63 (bases 1 to 27)	64 (bases 1 to 27)	65 (bases 1 to 27)	66 (bases 1 to 27)	67 (bases 1 to 27)	68 (bases 1 to 27)	69 (bases 1 to 27)	70 (bases 1 to 27)	71 (bases 1 to 27)	72 (bases 1 to 27)	73 (bases 1 to 27)	74 (bases 1 to 27)	75 (bases 1 to 27)	76 (bases 1 to 27)	77 (bases 1 to 27)	78 (bases 1 to 27)	79 (bases 1 to 27)	80 (bases 1 to 27)	81 (bases 1 to 27)	82 (bases 1 to 27)	83 (bases 1 to 27)	84 (bases 1 to 27)	85 (bases 1 to 27)	86 (bases 1 to 27)	87 (bases 1 to 27)	88 (bases 1 to 27)	89 (bases 1 to 27)	90 (bases 1 to 27)	91 (bases 1 to 27)	92 (bases 1 to 27)	93 (bases 1 to 27)	94 (bases 1 to 27)	95 (bases 1 to 27)	96 (bases 1 to 27)	97 (bases 1 to 27)	98 (bases 1 to 27)	99 (bases 1 to 27)	100 (bases 1 to 27)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
AUTHORS	Hecker, P.H. and Green, G.R.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						

504	10.6	39.3	30	6	AR142236	AR142236 Sequence 34
505	10.6	39.3	30	6	AR142237	AR142237 Sequence 34
506	10.6	39.3	30	6	AR142238	AR142238 Sequence 34
507	10.6	39.3	30	6	AR142239	AR142239 Sequence 34
508	10.6	39.3	30	6	AR142240	AR142240 Sequence 34
509	10.6	39.3	30	6	AR142241	AR142241 Sequence 34
510	10.6	39.3	30	6	AR142242	AR142242 Sequence 34
511	10.6	39.3	30	6	AR142243	AR142243 Sequence 34
512	10.6	39.3	30	6	AR142244	AR142244 Sequence 34
513	10.6	39.3	30	6	AR142245	AR142245 Sequence 34
514	10.6	39.3	30	6	AR142246	AR142246 Sequence 34
515	10.6	39.3	30	6	AR142247	AR142247 Sequence 34
516	10.6	39.3	30	6	AR142248	AR142248 Sequence 34
517	10.6	39.3	30	6	AR142249	AR142249 Sequence 34
518	10.6	39.3	30	6	AR142250	AR142250 Sequence 34
519	10.6	39.3	30	6	AR142251	AR142251 Sequence 34
520	10.6	39.3	30	6	AR142252	AR142252 Sequence 34
521	10.6	39.3	30	6	AR142253	AR142253 Sequence 34
522	10.6	39.3	30	6	AR142254	AR142254 Sequence 34
523	10.6	39.3	30	6	AR142255	AR142255 Sequence 34
524	10.6	39.3	30	6	AR142256	AR142256 Sequence 34
525	10.6	39.3	30	6	AR142257	AR142257 Sequence 34
526	10.6	39.3	30	6	AR142258	AR142258 Sequence 34
527	10.6	39.3	30	6	AR142259	AR142259 Sequence 34
528	10.6	39.3	30	6	AR142260	AR142260 Sequence 34
529	10.6	39.3	30	6	AR142261	AR142261 Sequence 34
530	10.6	39.3	30	6	AR142262	AR142262 Sequence 34
531	10.6	39.3	30	6	AR142263	AR142263 Sequence 34
532	10.6	39.3	30	6	AR142264	AR142264 Sequence 34
533	10.6	39.3	30	6	AR142265	AR142265 Sequence 34
534	10.6	39.3	30	6	AR142266	AR142266 Sequence 34
535	10.6	39.3	30	6	AR142267	AR142267 Sequence 34
536	10.6	39.3	30	6	AR142268	AR142268 Sequence 34
537	10.6	39.3	30	6	AR142269	AR142269 Sequence 34
538	10.6	39.3	30	6	AR142270	AR142270 Sequence 34
539	10.6	39.3	30	6	AR142271	AR142271 Sequence 34
540	10.6	39.3	30	6	AR142272	AR142272 Sequence 34
541	10.6	39.3	30	6	AR142273	AR142273 Sequence 34
542	10.6	39.3	30	6	AR142274	AR142274 Sequence 34
543	10.6	39.3	30	6	AR142275	AR142275 Sequence 34
544	10.6	39.3	30	6	AR142276	AR142276 Sequence 34
545	10.6	39.3	30	6	AR142277	AR142277 Sequence 34
546	10.6	39.3	30	6	AR142278	AR142278 Sequence 34
547	10.6	39.3	30	6	AR142279	AR142279 Sequence 34
548	10.6	39.3	30	6	AR142280	AR142280 Sequence 34
549	10.6	39.3	30	6	AR142281	AR142281 Sequence 34
550	10.6	39.3	30	6	AR142282	AR142282 Sequence 34
551	10.6	39.3	30	6	AR142283	AR142283 Sequence 34
552	10.6	39.3	30	6	AR142284	AR142284 Sequence 34
553	10.6	39.3	30	6	AR142285	AR142285 Sequence 34
554	10.6	39.3	30	6	AR142286	AR142286 Sequence 34
555	10.6	39.3	30	6	AR142287	AR142287 Sequence 34
556	10.6	39.3	30	6	AR142288	AR142288 Sequence 34
557	10.6	39.3	30	6	AR142289	AR142289 Sequence 34
558	10.6	39.3	30	6	AR142290	AR142290 Sequence 34
559	10.6	39.3	30	6	AR142291	AR142291 Sequence 34
560	10.6	39.3	30	6	AR142292	AR142292 Sequence 34
561	10.6	39.3	30	6	AR142293	AR142293 Sequence 34
562	10.6	39.3	30	6	AR142294	AR142294 Sequence 34
563	10.6	39.3	30	6	AR142295	AR142295 Sequence 34
564	10.6	39.3	30	6	AR142296	AR142296 Sequence 34
565	10.6	39.3	30	6	AR142297	AR142297 Sequence 34
566	10.6	39.3	30	6	AR142298	AR142298 Sequence 34
567	10.6	39.3	30	6	AR142299	AR142299 Sequence 34
568	10.6	39.3	30	6	AR142300	AR142300 Sequence 34
569	10.6	39.3	30	6	AR142301	AR142301 Sequence 34
570	10.6	39.3	30	6	AR142302	AR142302 Sequence 34
571	10.6	39.3	30	6	AR142303	AR142303 Sequence 34
572	10.6	39.3	30	6	AR142304	AR142304 Sequence 34
573	10.6	39.3	30	6	AR142305	AR142305 Sequence 34
574	10.6	39.3	30	6	AR142306	AR142306 Sequence 34
575	10.6	39.3	30	6	AR142307	AR142307 Sequence 34
576	10.6	39.3	30	6	AR142308	AR142308 Sequence 34

some better than others to the scope of the result. For example, the analysis of the total food distribution and of livestock analysis of the food distribution.

ON nucleic - nucleic search, using sw model

Rec'd on: July 21, 2003, 10:34:27. Sent to the SEC on: September 30, 2003.

2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818 2819 2820 2821 2822 2823 2824 2825 2826 2827 2828 2829 2830 2831 2832 2833 2834 2835 2836 2837 2838 2839 2840 2841 2842 2843 2844 2845 2846 2847 2848 2849 2850 2851 2852 2853 2854 2855 2856 2857 2858 2859 2860 2861 2862 2863 2864 2865 2866 2867 2868 2869 2870 2871 2872 2873 2874 2875 2876 2877 2878 2879 2880 2881 2882 2883 2884 2885 2886 2887 2888 2889 2890 2891 2892 2893 2894 2895 2896 2897 2898 2899 2900 2901 2902 2903 2904 2905 2906 2907 2908 2909 2910 2911 2912 2913 2914 2915 2916 2917 2918 2919 2920 2921 2922 2923 2924 2925 2926 2927 2928 2929 2930 2931 2932 2933 2934 2935 2936 2937 2938 2939 2940 2941 2942 2943 2944 2945 2946 2947 2948 2949 2950 2951 2952 2953 2954 2955 2956 2957 2958 2959 2960 2961 2962 2963 2964 2965 2966 2967 2968 2969 2970 2971 2972 2973 2974 2975 2976 2977 2978 2979 2980 2981 2982 2983 2984 2985 2986 2987 2988 2989 2990 2991 2992 2993 2994 2995 2996 2997 2998 2999 3000 3001 3002 3003 3004 3005 3006 3007 3008 3009 3010 3011 3012 3013 3014 3015 3016 3017 3018 3019 3020 3021 3022 3023 3024 3025 3026 3027 3028 3029 3030 3031 3032 3033 3034 3035 3036 3037 3038 3039 3040 3041 3042 3043 3044 3045 3046 3047 3048 3049 3050 3051 3052 3053 3054 3055 3056 3057 3058 3059 3060 3061 3062 3063 3064 3065 3066 3067 3068 3069 3070 3071 3072 3073 3074 3075 3076 3077 3078 3079 3080 3081 3082 3083 3084 3085 3086 3087 3088 3089 3090 3091 3092 3093 3094 3095 3096 3097 3098 3099 3100 3101 3102 3103 3104 3105 3106 3107 3108 3109 3110 3111 3112 3113 3114 3115 3116 3117 3118 3119 3120 3121 3122 3123 3124 3125 3126 3127 3128 3129 3130 3131 3132 3133 3134 3135 3136 3137 3138 3139 3140 3141 3142 3143 3144 3145 3146 3147 3148 3149 3150 3151 3152 3153 3154 3155 3156 3157 3158 3159 3160 3161 3162 3163 3164 3165 3166 3167 3168 3169 3170 3171 3172 3173 3174 3175 3176 3177 3178 3179 3180 3181 3182 3183 3184 3185 3186 3187 3188 3189 3190 3191 3192 3193 3194 3195 3196 3197 3198 3199 3200 3201 3202 3203 3204 3205 3206 3207 3208 3209 3210 3211 3212 3213 3214 3215 3216 3217 3218 3219 3220 3221 3222 3223 3224 3225 3226 3227 3228 3229 3230 3231 3232 3233 3234 3235 3236 3237 3238 3239 3240 3241 3242 3243 3244 3245 3246 3247 3248 3249 3250 3251 3252 3253 3254 3255 3256 3257 3258 3259 3260 3261 3262 3263 3264 3265 3266 3267 3268 3269 3270 3271 3272 3273 3274 3275 3276 3277 3278 3279 3280 3281 3282 3283 3284 3285 3286 3287 3288 3289 3290 3291 3292 3293 3294 3295 3296 3297 3298 3299 3300 3301 3302 3303 3304 3305 3306 3307 3308 3309 3310 3311 3312 3313 3314 3315 3316 3317 3318 3319 3320 3321 3322 3323 3324 3325 3326 3327 3328 3329 3330 3331 3332 3333 3334 3335 3336 3337 3338 3339 3340 3341 3342 3343 3344 3345 3346 3347 3348 3349 3350 3351 3352 3353 3354 3355 3356 3357 3358 3359 3360 3361 3362 3363 3364 3365 3366 3367 3368 3369 3370 3371 3372 3373 3374 3375 3376 3377 3378 3379 3380 3381 3382 3383 3384 3385 3386 3387 3388 3389 3390 3391 3392 3393 3394 3395 3396 3397 3398 3399 3400 3401 3402 3403 3404 3405 3406 3407 3408 3409 3410 3411 3412 3413 3414 3415 3416 3417 3418 3419 3420 3421 3422 3423 3424 3425 3426 3427 3428 3429 3430 3431 3432 3433 3434 3435 3436 3437 3438 3439 3440 3441 3442 3443 3444 3445 3446 3447 3448 3449 3450 3451 3452 3453 3454 3455 3456 3457 3458 3459 3460 3461 3462 3463 3464 3465 3466 3467 3468 3469 3470 3471 3472 3473 3474 3475 3476 3477 3478 3479 3480 3481 3482 3483 3484 3485 3486 3487 3488 3489 3490 3491 3492 3493 3494 3495 3496 3497 3498 3499 3500 3501 3502 3503 3504 3505 3506 3507 3508 3509 3510 3511 3512 3513 3514 3515 3516 3517 3518 3519 3520 3521 3522 3523 3524 3525 3526 3527 3528 3529 3530 3531 3532 3533 3534 3535 3536 3537 3538 3539 3540 3541 3542 3543 3544 3545 3546 3547 3548 3549 3550 3551 3552 3553 3554 3555 3556 3557 3558 3559 3560 3561 3562 3563 3564 3565 3566 3567 3568 3569 3570 3571 3572 3573 3574 3575 3576 3577 3578 3579 3580 3581 3582 3583 3584 3585 3586 3587 3588 3589 3590 3591 3592 3593 3594 3595 3596 3597 3598 3599 3600 3601 3602 3603 3604 3605 3606 3607 3608 3609 3610 3611 3612 3613 3614 3615 3616 3617 3618 3619 3620

FILED
DEC 1 1964
FBI - MEMPHIS

Sequence: 1 t c t j i g j h e r o s s e

Sorting table: IDENTIFY - NOC

6677-78

750
 760
 770
 780
 790
 800
 810
 820
 830
 840
 850
 860
 870
 880
 890
 900
 910
 920
 930
 940
 950
 960
 970
 980
 990
 1000
 1010
 1020
 1030
 1040
 1050
 1060
 1070
 1080
 1090
 1100
 1110
 1120
 1130
 1140
 1150
 1160
 1170
 1180
 1190
 1200
 1210
 1220
 1230
 1240
 1250
 1260
 1270
 1280
 1290
 1300
 1310
 1320
 1330
 1340
 1350
 1360
 1370
 1380
 1390
 1400
 1410
 1420
 1430
 1440
 1450
 1460
 1470
 1480
 1490
 1500
 1510
 1520
 1530
 1540
 1550
 1560
 1570
 1580
 1590
 1600
 1610
 1620
 1630
 1640
 1650
 1660
 1670
 1680
 1690
 1700
 1710
 1720
 1730
 1740
 1750
 1760
 1770
 1780
 1790
 1800
 1810
 1820
 1830
 1840
 1850
 1860
 1870
 1880
 1890
 1900
 1910
 1920
 1930
 1940
 1950
 1960
 1970
 1980
 1990
 2000
 2010
 2020
 2030
 2040
 2050
 2060
 2070
 2080
 2090
 2100
 2110
 2120
 2130
 2140
 2150
 2160
 2170
 2180
 2190
 2200
 2210
 2220
 2230
 2240
 2250
 2260
 2270
 2280
 2290
 2300
 2310
 2320
 2330
 2340
 2350
 2360
 2370
 2380
 2390
 2400
 2410
 2420
 2430
 2440
 2450
 2460
 2470
 2480
 2490
 2500
 2510
 2520
 2530
 2540
 2550
 2560
 2570
 2580
 2590
 2600
 2610
 2620
 2630
 2640
 2650
 2660
 2670
 2680
 2690
 2700
 2710
 2720
 2730
 2740
 2750
 2760
 2770
 2780
 2790
 2800
 2810
 2820
 2830
 2840
 2850
 2860
 2870
 2880
 2890
 2900
 2910
 2920
 2930
 2940
 2950
 2960
 2970
 2980
 2990
 3000
 3010
 3020
 3030
 3040
 3050
 3060
 3070
 3080
 3090
 3100
 3110
 3120
 3130
 3140
 3150
 3160
 3170
 3180
 3190
 3200
 3210
 3220
 3230
 3240
 3250
 3260
 3270
 3280
 3290
 3300
 3310
 3320
 3330
 3340
 3350
 3360
 3370
 3380
 3390
 3400
 3410
 3420
 3430
 3440
 3450
 3460
 3470
 3480
 3490
 3500
 3510
 3520
 3530
 3540
 3550
 3560
 3570
 3580
 3590
 3600
 3610
 3620
 3630
 3640
 3650
 3660
 3670
 3680
 3690
 3700
 3710
 3720
 3730
 3740
 3750
 3760
 3770
 3780
 3790
 3800
 3810
 3820
 3830
 3840
 3850
 3860
 3870
 3880
 3890
 3900
 3910
 3920
 3930
 3940
 3950
 3960
 3970
 3980
 3990
 4000
 4010
 4020
 4030
 4040
 4050
 4060
 4070
 4080
 4090
 4100
 4110
 4120
 4130
 4140
 4150
 4160
 4170
 4180
 4190
 4200
 4210
 4220
 4230
 4240
 4250
 4260
 4270
 4280
 4290
 4300
 4310
 4320
 4330
 4340
 4350
 4360
 4370
 4380
 4390
 4400
 4410
 4420
 4430
 4440
 4450
 4460
 4470
 4480
 4490
 4500
 4510
 4520
 4530
 4540
 4550
 4560
 4570
 4580
 4590
 4600
 4610
 4620
 4630
 4640
 4650
 4660
 4670
 4680
 4690
 4700
 4710
 4720
 4730
 4740
 4750
 4760
 4770
 4780
 4790
 4800
 4810
 4820
 4830
 4840
 4850
 4860
 4870
 4880
 4890
 4900
 4910
 4920
 4930
 4940
 4950
 4960
 4970
 4980
 4990
 5000
 5010
 5020
 5030
 5040
 5050
 5060
 5070
 5080
 5090
 5100
 5110
 5120
 5130
 5140
 5150
 5160
 5170
 5180
 5190
 5200
 5210
 5220
 5230
 5240
 5250
 5260
 5270
 5280
 5290
 5300
 5310
 532

[illegible]

Maximum seq length: 0

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

100

listing first 1000 subscribers

Conclusions

GenEmbl: *

$$2: \quad \frac{g^2}{q^2} \rightarrow \frac{g^2}{q^2} + \frac{g^2}{q^2}$$

4: qb cm.

100-1000

8 : 7 : 6 : 5 : 4 : 3 : 2 : 1

```
9: qb pr:
10:
```

11: qb-st
12: sy

13: sub-ur

15: cm-4.3

17: em_hu

19: evn_mu

21: cm^{-1} 22. cm⁻¹ F₂[illegible]

50

20. 2011. 12. 1.

31.

33: em_hc

35	3
34	4
33	5
32	6
31	7
30	8
29	9
28	10
27	11
26	12
25	13
24	14
23	15
22	16
21	17
20	18
19	19
18	20
17	21
16	22
15	23
14	24
13	25
12	26
11	27
10	28
9	29
8	30
7	31
6	32
5	33
4	34
3	35
2	36
1	37

3	3
2	0
1	1
0	1
3	3
2	2
1	1
0	0

em - 11

40: em_in
41: em_in

1. *Phragmites australis*
 2. *Scirpus americanus*
 3. *Spartina patens*
 4. *Distichlis spicata*
 5. *Eleocharis acicularis*
 6. *Eleocharis obtusa*
 7. *Eleocharis tenuis*
 8. *Eleocharis palustris*
 9. *Eleocharis acicularis*
 10. *Eleocharis obtusa*
 11. *Eleocharis tenuis*
 12. *Eleocharis palustris*
 13. *Eleocharis acicularis*
 14. *Eleocharis obtusa*
 15. *Eleocharis tenuis*
 16. *Eleocharis palustris*
 17. *Eleocharis acicularis*
 18. *Eleocharis obtusa*
 19. *Eleocharis tenuis*
 20. *Eleocharis palustris*
 21. *Eleocharis acicularis*
 22. *Eleocharis obtusa*
 23. *Eleocharis tenuis*
 24. *Eleocharis palustris*
 25. *Eleocharis acicularis*
 26. *Eleocharis obtusa*
 27. *Eleocharis tenuis*
 28. *Eleocharis palustris*
 29. *Eleocharis acicularis*
 30. *Eleocharis obtusa*
 31. *Eleocharis tenuis*
 32. *Eleocharis palustris*
 33. *Eleocharis acicularis*
 34. *Eleocharis obtusa*
 35. *Eleocharis tenuis*
 36. *Eleocharis palustris*
 37. *Eleocharis acicularis*
 38. *Eleocharis obtusa*
 39. *Eleocharis tenuis*
 40. *Eleocharis palustris*
 41. *Eleocharis acicularis*
 42. *Eleocharis obtusa*
 43. *Eleocharis tenuis*
 44. *Eleocharis palustris*
 45. *Eleocharis acicularis*
 46. *Eleocharis obtusa*
 47. *Eleocharis tenuis*
 48. *Eleocharis palustris*
 49. *Eleocharis acicularis*
 50. *Eleocharis obtusa*
 51. *Eleocharis tenuis*
 52. *Eleocharis palustris*
 53. *Eleocharis acicularis*
 54. *Eleocharis obtusa*
 55. *Eleocharis tenuis*
 56. *Eleocharis palustris*
 57. *Eleocharis acicularis*
 58. *Eleocharis obtusa*
 59. *Eleocharis tenuis*
 60. *Eleocharis palustris*
 61. *Eleocharis acicularis*
 62. *Eleocharis obtusa*
 63. *Eleocharis tenuis*
 64. *Eleocharis palustris*
 65. *Eleocharis acicularis*
 66. *Eleocharis obtusa*
 67. *Eleocharis tenuis*
 68. *Eleocharis palustris*
 69. *Eleocharis acicularis*
 70. *Eleocharis obtusa*
 71. *Eleocharis tenuis*
 72. *Eleocharis palustris*
 73. *Eleocharis acicularis*
 74. *Eleocharis obtusa*
 75. *Eleocharis tenuis*
 76. *Eleocharis palustris*
 77. *Eleocharis acicularis*
 78. *Eleocharis obtusa*
 79. *Eleocharis tenuis*
 80. *Eleocharis palustris*
 81. *Eleocharis acicularis*
 82. *Eleocharis obtusa*
 83. *Eleocharis tenuis*
 84. *Eleocharis palustris*
 85. *Eleocharis acicularis*
 86. *Eleocharis obtusa*
 87. *Eleocharis tenuis*
 88. *Eleocharis palustris*
 89. *Eleocharis acicularis*
 90. *Eleocharis obtusa*
 91. *Eleocharis tenuis*
 92. *Eleocharis palustris*
 93. *Eleocharis acicularis*
 94. *Eleocharis obtusa*
 95. *Eleocharis tenuis*
 96. *Eleocharis palustris*
 97. *Eleocharis acicularis*
 98. *Eleocharis obtusa*
 99. *Eleocharis tenuis*
 100. *Eleocharis palustris*

1000000

with adapters complementary to the insert adapters and purified. The sheared, adaptered mouse DNA was annealed to adaptered vector DNA, and transformed into chemically-competent *E. coli* Xho-3d3 (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT	14 d	10 c	3 q	2 t
ORIGIN				

ORIGIN

Query Match	38.78	Score 11.6	DB 17	Length 29
Best Local Similarity	77.8	Pred. No. 1.3e+06		
Matches 14	Conservative 0	Mismatches 4	Indels 0	Gaps 0

QY 5 AGAGACACCAAGACACT 22

9 ACACACAAAGATACT 26

Search completed: July 21, 2003, 15:47:29
Job time : 799.76 secs

ACCESSION HT59548
VERSION 010002987
FEATURES
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

HT59548
01-10-2002
fruit fly
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Euryptera;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bflytricheta; Drosophilinae; Drosophilini
1 (bases 1 to 25)
Lewis, R.; Hoskins, P.; Liang, G.; Morgan, N.; Tsang, G.; He, Y.; Kapen,
G.; Ballou, H.; Pabinger, G. and Stralinger, A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-1200, USA
Fax: 5106443947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 19 in the 25 bases. This
insertion position refers to the first base of the a base target
recognition sequence
Class: Transposon-tagged
Location/Qualifiers
1..25
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/feature_1b="Transfected from parent P[19794] P element
insertion lines"
/note="Inverse-PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P[SOX] P element. Inverse-PCR was used to determine the location
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
<http://www.fruitfly.org/about/methods/inverse-pcr.html>."

BASE COUNT
ORIGIN
1 a 7 c 8 g 7 t

Query March 40 78, Score 12.3, DP 17, Length 75,
Best Local Similarity 60.48, Pval 0.000000
Matches 14, Conservative 0, Mismatches 7, Indels 0, Gaps 0

QY 1 GCGAAGATACGCTAAG 17
|||||
25 GCGAAGATACGCTAAG 9

RESULT 19
LOCUS
DEFINITION
AUTHORS
TITLE
JOURNAL
COMMENT

AA665891 28 bp mRNA linear EST 13-MAR-1998
Characterized from a cDNA library from a mouse embryo (AA665891) and
similar to the cDNA from a mouse embryo (AA665891) from a mouse embryo
L1 repetitive element. mRNA sequence
AA665891
AA665891 1 nt 1000000
EST
Human
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Vertebrata; Eumetazoa;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
1 (bases 1 to 28)
NCI-NCAT <http://www.ncbi.nlm.nih.gov/ncat/>
National Cancer Institute, Cancer Therapy Evaluation Program (CTEP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@ncat.nih.gov
Tissue Procurement: Christopher Moevalle, M.D., Ph.D., Michael R.
Emmett-Ruck, M.D., Ph.D.

ACCESSION HT59548
VERSION 010002987
FEATURES
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

HT59548
01-10-2002
fruit fly
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Euryptera;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bflytricheta; Drosophilinae; Drosophilini
1 (bases 1 to 25)
Lewis, R.; Hoskins, P.; Liang, G.; Morgan, N.; Tsang, G.; He, Y.; Kapen,
G.; Ballou, H.; Pabinger, G. and Stralinger, A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-1200, USA
Fax: 5106443947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 19 in the 25 bases. This
insertion position refers to the first base of the a base target
recognition sequence
Class: Transposon-tagged
Location/Qualifiers
1..25
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/feature_1b="Transfected from parent P[19794] P element
insertion lines"
/note="Inverse-PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P[SOX] P element. Inverse-PCR was used to determine the location
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
<http://www.fruitfly.org/about/methods/inverse-pcr.html>."

BASE COUNT
ORIGIN
1 a 7 c 8 g 7 t

Query March 40 78, Score 12.3, DP 17, Length 75,
Best Local Similarity 60.48, Pval 0.000000
Matches 14, Conservative 0, Mismatches 7, Indels 0, Gaps 0

QY 1 GCGAAGATACGCTAAG 17
|||||
25 GCGAAGATACGCTAAG 9

RESULT 20
LOCUS
DEFINITION
AUTHORS
TITLE
JOURNAL
COMMENT

AA665891 28 bp mRNA linear EST 13-MAR-1998
Characterized from a cDNA library from a mouse embryo (AA665891) and
similar to the cDNA from a mouse embryo (AA665891) from a mouse embryo
L1 repetitive element. mRNA sequence
AA665891
AA665891 1 nt 1000000
EST
Human
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Vertebrata; Eumetazoa;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
1 (bases 1 to 28)
NCI-NCAT <http://www.ncbi.nlm.nih.gov/ncat/>
National Cancer Institute, Cancer Therapy Evaluation Program (CTEP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@ncat.nih.gov
Tissue Procurement: Christopher Moevalle, M.D., Ph.D., Michael R.
Emmett-Ruck, M.D., Ph.D.

[illegible]

: APPLICANT: Miltman, Michael
 : TITLE OF INVENTION: Human Microarray
 : FILE REFERENCE: 3118.1
 : CURRENT APPLICATION NUMBER: US/19/098,263B
 : CURRENT FILING DATE: 2003-01-08
 : PRIOR APPLICATION NUMBER: 08/226,759
 : PRIOR FILING DATE: 2001-03-16
 : NUMBER OF SEQ ID NOS: 131066
 : SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 : SEQ ID NO: 81311
 : LENGTH: 25
 : TYPE: DNA
 : ORGANISM: Homo sapien
 : US-10 098 263B-81311

Query Match 48.7% Score 14.6; DB 15; Length 25;
 Best local Similarity 81.0%; Pred. No. 6.5e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 C1 4 AATAATACCAATACACTAC 24
 ||||| ||||| |||||
 Mb 2 AATAGCTGTCAACACCACTAC 22

Search completed: July 21, 2003, 18:48:21
 Job time : 81.6397 secs

Matches 13, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000

QY 3 CACAGACAGACAGACAGACAGACAG 25
 DB 2 CACAGACAGACAGACAGACAGACAG 24

RESULT 35
 US-10-098-263B-24248
 Sequence 24248, Application US/10098263B
 Publication No. US20030100001
 GENERAL INFORMATION:
 APPLICANT: Bayer, Kevin P.
 APPLICANT: Betsch, David
 APPLICANT: Deschamps, Luc
 APPLICANT: Eason, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fogli, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Ashley
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gunney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Hu, James
 APPLICANT: Paoletti, Nicholas F.
 TITLE OF INVENTION: Secreted and Transcribed RNA Interference and Methods
 FILE REFERENCE: P28901061
 CURRENT APPLICATION NUMBER: US/2003/0100001
 CURRENT FILING DATE: 2002-06-25
 PRIOR APPLICATION removed - See File Wrapper of P28901061
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 294
 LENGTH: 24
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide
 US-10-098-263B-24248

QY 3 CACAGACAGACAGACAGACAGACAG 25
 DB 2 CACAGACAGACAGACAGACAGACAG 24

Matches 18, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000

RESULT 37
 US-10-098-263B-24248
 Sequence 24248, Application US/10098263B
 Publication No. US20030100001
 GENERAL INFORMATION:
 APPLICANT: Mittman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 09/076,799
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 191066
 SOFTWARE: Microarray Probe Sequence Listing Description V 1.1
 SEQ ID NO 24248
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-098-263B-24248

Query Match 49.3% Score 14.87 DB 15 Length 251
 Best Local Similarity 99.0% File No. 5.44e+03
 Matches 16, Conservative 3, Mismatches 1, Indels 0, Gaps 0

QY 8 GACACAGACAGACAGACAGACAG 25
 DB 5 GACACAGACAGACAGACAGACAG 25

RESULT 38
 US-10-098-263B-39065
 Sequence 39065, Application US/10098263B
 Publication No. US20030100001
 GENERAL INFORMATION:
 APPLICANT: Mittman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 09/076,799
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 39065
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-098-263B-39065

Query Match 13.3% Score 11.93 DB 15 Length 251
 Best Local Similarity 52.0% File No. 5.44e+03
 Matches 16, Conservative 2, Mismatches 2, Indels 0, Gaps 0

QY 10 CACACAGACAGACAGACAGACAG 27
 DB 3 CACACAGACAGACAGACAGACAG 25

RESULT 39
 US-09-216-393-220
 Sequence 393, Application US/09216393
 Publication No. US20010144741
 GENERAL INFORMATION:
 APPLICANT: Milhausen, Michael James
 TITLE OF INVENTION: Translational Repression, Methods and Compositions
 FILE REFERENCE: TX 102
 CURRENT APPLICATION NUMBER: US/09/216,393
 CURRENT FILING DATE: 1998-12-18
 EARLIER APPLICATION NUMBER: 09/094,935
 PRIOR FILING DATE: 1997-12-19
 NUMBER OF SEQ ID NOS: 364
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 220
 LENGTH: 23
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Primer
 US-09-216-393-220

Query Match 49.3% Score 14.6 DB 15 Length 231
 Best Local Similarity 81.0% File No. 6.44e+03
 Matches 17, Conservative 0, Mismatches 4, Indels 0, Gaps 0

QY 7 AACACAGACAGACAGACAGACAG 27
 DB 1 AACACAGACAGACAGACAGACAG 21

RESULT 40
 US-10-098-263B-81311
 Sequence 81311, Application US/10098263B
 Publication No. US20030100001
 GENERAL INFORMATION:


```

Sequence 294, Application US/10011002A
Publication No. US20040109672A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Ian I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paret, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P28010160
CURRENT FILING DATE: 2001-12-07
Prior application removed - see file wrapper of Paim
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 294
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by Gene-Screen Plus
US 10 011 602A 294
Query Match 50.0% Score 150 DB 150 Length 240
Best Local Similarity 78.1% Pct 4.4e-03
Matches 18; Conservative 0; Mismatches 5; Indels 0; Infs 0
CY 3 CAAAGACAGCTAAAGACAGCTAC 25
10 2 CAAAGACAGCTAAAGACAGCTAC 24
RESULT 41
US-10-006-768A-294
Sequence 294, Application US/10011002A
Publication No. US20040109672A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Paret, Nicholas F.
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Ian I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paret, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P28010160
CURRENT FILING DATE: 2001-12-07
Prior application removed - see file wrapper of Paim
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 294
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by Gene-Screen Plus

```

```

US-10-006-768A-294
Query Match 50.0% Score 150 DB 150 Length 240
Best Local Similarity 78.1% Pct 4.4e-03
Matches 18; Conservative 0; Mismatches 5; Indels 0; Infs 0
CY 3 CAAAGACAGCTAAAGACAGCTAC 25
10 2 CAAAGACAGCTAAAGACAGCTAC 24
RESULT 32
US-10-017-610A-294
Sequence 294, Application US/10011002A
Publication No. US20040109672A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Paret, Nicholas F.
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Ian I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paret, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P28010160
CURRENT FILING DATE: 2001-12-13
Prior application removed - see file wrapper of Paim
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 294
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by Gene-Screen Plus
US 10 017 610A 294
Query Match 50.0% Score 150 DB 150 Length 240
Best Local Similarity 78.1% Pct 4.4e-03
Matches 18; Conservative 0; Mismatches 5; Indels 0; Infs 0
CY 3 CAAAGACAGCTAAAGACAGCTAC 25
10 2 CAAAGACAGCTAAAGACAGCTAC 24
RESULT 32
US-10-017-610A-294
Sequence 294, Application US/10011002A
Publication No. US20040109672A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Paret, Nicholas F.
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Ian I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paret, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P28010160
CURRENT FILING DATE: 2001-12-13
Prior application removed - see file wrapper of Paim
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 294
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by Gene-Screen Plus

```


[illegible]

```

1  PRIC AFFILIATION NUMBER: 607106902
2  PRIC FILING DATE: 1998-10-26
3  PRIC AFFILIATION NUMBER: 607106904
4  PRIC FILING DATE: 1998-10-26
5  PRIC AFFILIATION NUMBER: 607106907
6  PRIC FILING DATE: 1998-10-27
7  PRIC AFFILIATION NUMBER: 607106901
8  PRIC FILING DATE: 1998-10-27
9  PRIC AFFILIATION NUMBER: 607106902
10 PRIC FILING DATE: 1998-10-27
11 PRIC AFFILIATION NUMBER: 607106923
12 PRIC FILING DATE: 1998-10-28
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997

```


APPLICANT, ESTHER L. DAVIS

1. CHECK EILING DATE: 1997-03-16

[illegible]

```

      RESULT 17
      US-10-968-815A-294
      Date Recd: 124, Affiliation: NCIT/NCI-NIDA
      Publication No.: USZ0000054406A1
      GENERAL INFORMATION:
        APPLICANT: Baker, Kevin P.
        AFFILIANT: Rostein, David
        APPLICANT: Resnayer, Luc
        APPLICANT: Batou, Dan L.
        APPLICANT: Bellini, Raffaele
        APPLICANT: Ferry, Sherman
        APPLICANT: Jia, Wei-Chang
        APPLICANT: Johnson, Andrew
        APPLICANT: Grodzewski, Paul J.
        APPLICANT: Grimaldi, Christopher J.
        APPLICANT: Guiney, Austin L.
        APPLICANT: Hillan, Kenneth J.
        APPLICANT: Pan, James
        APPLICANT: Fazio, Nicholas F.
        TITLE OF INVENTION: Sequences of Transmembrane Polypeptides and Methods
        TITLE OF INVENTION: Acids Encoding the Same
        FILE REFERENCE: E280104
        CURRENT AFFILIATION NUMBER: NCIT/US/968-815A
        CURRENT FILING DATE: 2002-12-06
        Prior Application removed - see file wrapper at Palm
        SFO ID NO 294
        LENGTH: 24
        TYPE: DNA
        ORGANISM: Artificial Sequence
        FEATURE:
          OTHER INFORMATION: Synthetic oligonucleotide probe
          UN 10-906 815A-294
    Query Match      50-63; Sense 15; PE 15; Length 24;
    Best Local Similarity   80.3%; E-Val: Not Available;
    Matches 1st, Conservative 1; Mismatched 5; Info's
              3 CACATCAACAACAAGACTTACC 25
              ||||| | ||| | |
              4 CCACAAACGCGCATCAGCTTC 24

RESULT 18
UN 10-915-393A-294
Date Recd: 124, Affiliation: NCIT/NCI-NIDA
Publication No.: USZ0000054406A1
GENERAL INFORMATION:
  APPLICANT: Baker, Kevin P.
  AFFILIANT: Rostein, David
  APPLICANT: Resnayer, Luc
  APPLICANT: Batou, Dan L.
  APPLICANT: Bellini, Raffaele
  APPLICANT: Ferry, Sherman
  APPLICANT: Jia, Wei-Chang
  APPLICANT: Johnson, Andrew
  APPLICANT: Grodzewski, Paul J.
  APPLICANT: Grimaldi, Christopher J.
  APPLICANT: Guiney, Austin L.
  APPLICANT: Hillan, Kenneth J.
  APPLICANT: Pan, James
  APPLICANT: Fazio, Nicholas F.
  TITLE OF INVENTION: Sequences of Transmembrane Polypeptides and Methods
  TITLE OF INVENTION: Acids Encoding the Same
  FILE REFERENCE: E280104
  CURRENT AFFILIATION NUMBER: NCIT/US/915-393A
  CURRENT FILING DATE: 2002-06-10
  Prior Application removed - See file wrapper at Palm
  NUMBER OF SFO ID NOS: 477
  SFO ID NO 294

```

```

PRIORITY FILING DATE: 1998-10-07
PRIORITY APPLICATION NUMBER: 60/103335
PRIORITY FILING DATE: 1998-10-07
PRIORITY APPLICATION NUMBER: 60/103328
PRIORITY FILING DATE: 1998-10-07
PRIORITY APPLICATION NUMBER: 60/103395
PRIORITY FILING DATE: 1998-10-07
PRIORITY APPLICATION NUMBER: 60/103396
PRIORITY FILING DATE: 1998-10-07
PRIORITY APPLICATION NUMBER: 60/103401
PRIORITY FILING DATE: 1998-10-07
PRIORITY APPLICATION NUMBER: 60/103444
PRIORITY FILING DATE: 1998-10-06
PRIORITY APPLICATION NUMBER: 60/103451
PRIORITY FILING DATE: 1998-10-08
PRIORITY APPLICATION NUMBER: 60/103578
PRIORITY FILING DATE: 1998-10-08
PRIORITY APPLICATION NUMBER: 60/103704
PRIORITY FILING DATE: 1998-10-08
PRIORITY APPLICATION NUMBER: 60/103711
PRIORITY FILING DATE: 1998-10-08
PRIORITY APPLICATION NUMBER: 60/104257
PRIORITY FILING DATE: 1998-10-14
PRIORITY APPLICATION NUMBER: 60/104297
PRIORITY FILING DATE: 1998-10-20
PRIORITY APPLICATION NUMBER: 60/105000
PRIORITY FILING DATE: 1998-10-20
PRIORITY APPLICATION NUMBER: 60/105002
PRIORITY FILING DATE: 1998-10-20
PRIORITY APPLICATION NUMBER: 60/105104
PRIORITY FILING DATE: 1998-10-21
PRIORITY APPLICATION NUMBER: 60/105104
PRIORITY FILING DATE: 1998-10-22
PRIORITY APPLICATION NUMBER: 60/105200
PRIORITY FILING DATE: 1998-10-22
PRIORITY APPLICATION NUMBER: 60/105693
PRIORITY FILING DATE: 1998-10-26
PRIORITY APPLICATION NUMBER: 60/105694
PRIORITY FILING DATE: 1998-10-26
PRIORITY APPLICATION NUMBER: 60/105697

```

Query March 50.0% Score 15, EB 10, Length 24,
Best Local Similarity 78.3%, Freq No. 4,4e+03,
Matches 18, Conservative 5, Mismatches 5, Indels 0, Gaps 0.

```

CY 3 CAGAGACATCAAGACACTACG 25
DE 2 CAGAGACATCAAGACACTACG 24

```

RESULT 13
US-10-005-041A-294
Sequence 294, Application US/10015822A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bernstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth D.
APPLICANT: Pan, James
APPLICANT: Rasmussen, Nicholas F.
TITLE OF INVENTION: Methods and Transcription Factors Encoding the Same
FILE REFERENCE: P2810P1C
CURRENT APPLICATION NUMBER: US/10-005-041A

```

CURRENT FILING DATE: 2001-12-06
PRIORITY APPLICATION REMOVED - See File Wrapper or Page
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 294
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: You have selected the probe
US-10-005-041A-294

```

Query March 50.0% Score 15, EB 14, Length 24,
Best Local Similarity 78.3%, Freq No. 4,4e+03,
Matches 18, Conservative 5, Mismatches 5, Indels 0, Gaps 0.

```

CY 3 CAGAGACATCAAGACACTACG 25
DE 2 CAGAGACATCAAGACACTACG 24

```

RESULT 14
US-10-011-833A-294
Sequence 294, Application US/10011833A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bernstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth D.
APPLICANT: Pan, James
APPLICANT: Rasmussen, Nicholas F.
TITLE OF INVENTION: Methods and Transcription Factors Encoding the Same
FILE REFERENCE: P2830P1C2
CURRENT APPLICATION NUMBER: US/10-011-833A
PRIORITY FILING DATE: 2002-06-25
PRIORITY APPLICATION REMOVED - See File Wrapper or Page
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 294
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-833A-294

Query March 50.0% Score 15, EB 14, Length 24,
Best Local Similarity 78.3%, Freq No. 4,4e+03,
Matches 18, Conservative 5, Mismatches 5, Indels 0, Gaps 0.

```

CY 3 CAGAGACATCAAGACACTACG 25
DE 2 CAGAGACATCAAGACACTACG 24

```

RESULT 15
US-10-015-822A-294
Sequence 294, Application US/10015822A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bernstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone

Db 20 AGAGTACCAAGCAATCA 2

RESULT 9

US-09-864-029-53
 Publication No. US2003010410A1
 GENERAL INFORMATION:
 APPLICANT: Third Wave Technologies
 APPLICANT: Altmay, Haim
 APPLICANT: Eastholme, Christian
 APPLICANT: Chehak, LuAnne
 TITLE OF INVENTION: Detection of RNA Sequences
 FILE REFERENCE: POPS-04944
 CURRENT AFFILIATION NUMBER: US/09/004,636A
 PRIOR FILING DATE: 2001-02-26
 NUMBER OF SEQ ID NOS: 2540
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 167
 LENGTH: 10
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-864-636A-1567

Query Match 52.7% Score 15.8; DB 12; Length 30;
 Best Local Similarity 89.5%; Pred. No. 2,1e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGACGACCAAGCAAGCTCA 23
 Db 20 AGAGTACCAAGCAATCA 2

RESULT 10
 US-09-864-029-53
 Publication No. US2003010410A1
 GENERAL INFORMATION:
 APPLICANT: Pathogen, Michael
 APPLICANT: Szykew, Kimberly A
 APPLICANT: Majumder, Kumud
 APPLICANT: Tcherepov, Velizar T.
 APPLICANT: Grosz, William M.
 APPLICANT: Szekeres, Jr., Edward S
 APPLICANT: Alsobrook II, John P.
 APPLICANT: Burgess, Catherine E.
 APPLICANT: Shumaker, Richard A.
 APPLICANT: Touffier, Jr., Raymond J.
 APPLICANT: Casman, Stacie J.
 APPLICANT: Gaspoliti, Esda A.
 APPLICANT: Macdonald, John R.
 APPLICANT: Stone, David J.
 APPLICANT: Smithson, Glenda
 TITLE OF INVENTION: SEVER, SEB, LIFE, ISOLEUCINE AND NUCLEIC ACIDS ENCODING
 FILE REFERENCE: 21403,022
 CURRENT AFFILIATION NUMBER: 77-09-004,636A
 PRIOR FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/271,645
 PRIOR FILING DATE: 2000-05-24
 PRIOR APPLICATION NUMBER: 60/214,172
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 60/214,176
 PRIOR FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 60/207,920
 PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: 60/207,923
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: 60/215,742
 PRIOR FILING DATE: 2000-10-10

PRIOR APPLICATION NUMBER: 60/256,402
 PRIOR FILING DATE: 2000-10-18
 PRIOR APPLICATION NUMBER: 60/271,645
 PRIOR FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/274,809
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: 60/256,402
 PRIOR FILING DATE: 2001-03-13
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 53
 LENGTH: 22
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:
 OTHER INFORMATION: Cloning Vector
 US-09-864-029-53

Query Match 50.7% Score 15.2; DB 12; Length 22;
 Best Local Similarity 85.0%; Pred. No. 3,6e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CACCAACACTACCACTCA 29
 Db 3 CACCAACACTACCTCA 22

RESULT 11
 US-09-864-029-53
 Publication No. US2003010410A1
 GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 APPLICANT: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT AFFILIATION NUMBER: US/09/004,636A
 PRIOR FILING DATE: 2003-01-08
 FILE AFFILIATION NUMBER: 60/207,920
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequences Mapping Generator V.1.1
 SEQ ID NO: 29595
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-864-29595-29585

Query Match 50.7% Score 15.2; DB 15; Length 25;
 Best Local Similarity 85.0%; Pred. No. 3,7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGACGACCAAGCAAGCTCA 24
 Db 24 AGAGTACCAAGCAATCA 5

RESULT 12
 US-09-864-374-294
 Publication No. US2003010410A1
 GENERAL INFORMATION:
 APPLICANT: Bayer, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Esenzyer, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Festari, Napoleone
 APPLICANT: Peng, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Jodanis, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.

```

FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: Patentin version 3.0
SEQ ID NO 1561
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1551

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  AAGATGACCAAGACACCA 23
DB      20  AAGATGACCAAGACACCA 2

RESULT 5
US-09-864-636A-1554
Sequence: AAGATGACCAAGACACCA
Publication No: US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alkermes, Halim, Christian
APPLICANT: Bartholomew, Christian
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: Patentin version 3.0
SEQ ID NO 1554
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1554

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  AAGATGACCAAGACACCA 23
DB      20  AAGATGACCAAGACACCA 2

RESULT 6
US-09-864-636A-1557
Sequence: AAGATGACCAAGACACCA
Publication No: US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alkermes, Halim, Christian
APPLICANT: Bartholomew, Christian
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: Patentin version 3.0
SEQ ID NO 1557
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence

```

```

FEATURE:
US-09-864-636A-1557

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  AAGATGACCAAGACACCA 23
DB      20  AAGATGACCAAGACACCA 2

RESULT 7
US-09-864-636A-1561
Sequence: AAGATGACCAAGACACCA
Publication No: US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alkermes, Halim, Christian
APPLICANT: Bartholomew, Christian
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: Patentin version 3.0
SEQ ID NO 1561
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1561

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  AAGATGACCAAGACACCA 23
DB      20  AAGATGACCAAGACACCA 2

RESULT 8
US-09-864-636A-1561
Sequence: AAGATGACCAAGACACCA
Publication No: US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alkermes, Halim, Christian
APPLICANT: Bartholomew, Christian
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: Patentin version 3.0
SEQ ID NO 1564
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1564

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  AAGATGACCAAGACACCA 23

```


[illegible]

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/261,068
 FILING DATE: 16-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hsi, Patricia S
 REGISTRATION NUMBER: 38,496
 REFERENCE/DOCKET NUMBER: ED3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: rRNA
 ORIGINAL SOURCE:
 ORGANISM: Mycobacterium avium
 US-08-757-180-16

Query Match 41.38, Score 12.4, DE 1, Length 34,
 Best local Similarity 72.78; Pred. NO. 8.4e+03;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

CY 3 CAAGAGACCCAAAGACACTAC 24
 ||||| ||||| |||||
 Db 32 CAAGAGTTAAAGAAATTAAC 11

Search completed: July 21, 2003, 15:49:05
 Job time: 32.994 secs

RESULT 38
US-09-111-573-27

Sequence 27, Application US/09111573
Patent No. 6220363

GENERAL INFORMATION
APPLICANT: Kellough, Jill A.
APPLICANT: Beswick, Richard P.
TITLE OF INVENTION: PLANT TISSUE / SLICE SHEET FOR MONITORING
TITLE OF INVENTION: PATENTED EXHIBITION OF TRANSFORMED PLANTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:
MEDIA TYPE: Diskette
COMPUTED BY: PG DELINGER
CREATING SYSTEM: IBM
SOFTWARE: PARTSO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09111573
FILING DATE:

CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09111573
FILING DATE: 09 JAN 1997
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/CITATION NUMBER: 4,937,741
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0949
TELEFAX: (650) 324-0940

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: amplified from cDNA (Fig 2A)

Query Match 42 (v) Score 19 (v) PB 0 Length 35,
Best Local Similarity 66.7%, Freq 10.7%
Matches: 18 Conservative 0 Mismatches 0 Gaps 0

Db : EMBL/GenBank/DDB/Joint NCBI
AAAAAAAAAAAAAGAGCTGACGAGCCT 34

RESULT 39
US-09-111-573-27

Sequence 17, Application US/09111573
Patent No. 6220363

GENERAL INFORMATION:
APPLICANT: Britschgi, Theresa B.
APPLICANT: Cantelosi, Gerard A.
TITLE OF INVENTION: Rapid and Sensitive Detection of
TITLE OF INVENTION: Antibiotic-Resistant Microorganisms Using Nitroimidazole
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steady Street Tower

```

STATE: San Francisco  
COUNTRY: USA  
ZIP: 94108-1492
```

COMPUTER PROGRAMS FOR:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #106, Version #1.72
PARENT APPLICATION NAME: 387-7447-1
FILING DATE: 30-JUN-1994
CLASSIFICATION: 425

PRIOR APPLICATION DATA:
APPLICATION NUMBER: no 60761,068
FILING DATE: 16 JUN 1994
APPLICANT/AGENT INFORMATION:

NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/CHECK NUMBER: 149-7-1
INVENTORIAL INFORMATION:
TELEPHONE: (415) 543-9600
TELEX: (415) 543-5043
INFORMATION PER SEC II NO. 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
ISOLATION METHOD:
MOLECULE TYPE: RNA
ORIGINAL SOURCE:

FEATURES:
MAKE/REX: PEGUSAL_RNA
LOCATION: 4434
OTHER IDENTIFIERS /NOTES "I+RVA_pen region"

Query Match: 41.3% Score 12.9, DB 1, Length 34;
Post Local Similarity 72.7%; Prod No. 9,46+03;
Matches: 16, Conservative = Miscellaneous = Indels = Caps =

CHAATWACCAATACTGCG 24
||||| |||||
32 CAGAAATTAAAAGAATTTC 11

RESULT 40
US-08-757-180-16/c
Sequence 16 Application US/08757180
Parent No. 5720221
OFFICIAL INFORMATION:
APPLICANT: Bartschaj, Theresa E
APPLICANT: Gargelosi, Gerard A
TITLE OF INVENTION: FAULT TOLERANT MECHANISM FOR PRELIMINARY CONTACT
TITLE OF INVENTION: FINGERPRINT RUM DIFFERENCE FROM MYCOBACTERIUM
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Neave
STREET: 1231 Avenue of the Americas
City: New York
State: New York
Country: United States of America
Zip: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Patent Release #106, Version #1.72
CURRENT APPLICATION DATA:
AFFILIATION NUMBER: US/06/757180
FILING DATE: 23 May 1994
CLASSIFICATION: 435

RESULT 36
 US-08-592-9368-27
 Sequence-27, Applicant US/595529368
 Patent No. 5741341
 GENERAL INFORMATION:
 APPLICANT: POLYOTT, WILL A.
 APPLICANT: POLYOTT, RICHARD K.
 TITLE OF INVENTION: LEAST NUMBER OF STAGE AND TEST PROBLEMS FOR
 TITLE OF INVENTION, REGULATED EXPRESSION OF TRANSGENES IN PLANTS
 NUMBER OF SEQUENCES: 27
 CONTACT/SCIENCE ADDRESS:
 ADDRESSEE: Pollyott & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Falm Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94106
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Dos
 SOFTWARE: PASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/592,936B
 FILING DATE: 29 JAN 1996
 CLASSIFICATION: 600
 ATTORNEY/AGENT INFORMATION:
 NAME: Evans, Susan T.
 REGISTRATION NUMBER: 38,443
 REFERENCE TO OTHER PUBLICATIONS: 4,173,012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 324-0680
 TELEFAX: (650) 324-0690
 INFORMATION FOR SEQ. ID NO.: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

COMPILED READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEST for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 167087788.028A
FILING DATE: 24 JAN 1997
CLASSIFICATION: NO
PRICE APPLICATION DATA:
APPLICATION NUMBER: 167087788.036
FILING DATE: 23 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 18,443
REFERENCE/DOCKET NUMBER: 4257-0015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEC ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ORIGINATOR: amplified from cDNA T94 11A
ID: 29 168-028A 25

Unit Match	42/43	Score 12/6	DB 1	Length 103
Best Local Similarity	66.7%	Pred. No. 78403		
Matches	12	Conservative	0	Mismatches 0
4	AATGACACCCAAACAAATACCAACAT	30		
8	AAAAAAAAAAAAAGCTATCAAGAGCT	34		
DB				
QY				

33 CCAGATACCAAGGACCAATGATTA 3

RESULT 32

US-09-464-601-3

Sequence 2, Application US/08464601

Patent No. 6245940

GENERAL INFORMATION:

APPLICANT: HUSCON, ET AL.

TITLE OF INVENTION: Human Choline Acetyltransferase

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: CECCHI, ERMEN, BAIN, JEFFREY, A.

ADDRESSEE: CECCHI, STEWART & CLOSTEIN

STREET: 4 BRIDGE FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

CONVERTER RESEARCH FORM

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/08464601

FILING DATE: June 5, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/08464601

FILING DATE: 23 NOV 1994

AUTHOR/INVENTOR INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,7134

REFERENCE/DOC# NUMBER: 36890-333

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NOS: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 BASE PAIRS

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

MOLECULE TYPE: OLIGONUCLEOTIDE

US-08-464-601-3

Copy Match: 42.0%, Score 12.6, DP 4, Length 34

Best Local Similarity: 66.7%, Start No. 6, End No. 11

Mismatches: 19, Conservative: 0, Mismatched: 6, Indels: 0, Gaps: 0

2 CCAGATACCAAGGACCAATGATTA 25

2 CCAGATACCAAGGACCAATGATTA 29

RESULT 33

US-09-210-993A-3

Sequence 3, Application US/09210993A

Patent No. 6319700

GENERAL INFORMATION:

APPLICANT: Hudson, et al.

TITLE OF INVENTION: Human Choline Acetyltransferase

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 3113 Key West Ave

CITY: Rockville

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

CONVERTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.33

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/09210993A

FILING DATE: 10-Dec-1998

CLASSIFICATION: unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/09210993A

FILING DATE: 03-JUN-1995

APPLICATION NUMBER: 09/09210993A

FILING DATE: 23 NOV 1994

AUTHOR/INVENTOR INFORMATION:

NAME: BROOKES, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOC# NUMBER: 36146P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NOS: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: linear

SEQUENCE DESCRIPTION: SEQ ID NOS: 3:

US-09-210-993A-3

Copy Match: 42.0%, Score 12.6, DP 4, Length 34

Best Local Similarity: 66.7%, Start No. 6, End No. 11

Mismatches: 19, Conservative: 0, Mismatched: 6, Indels: 0, Gaps: 0

2 CCAGATACCAAGGACCAATGATTA 28

2 CCAGATACCAAGGACCAATGATTA 29

RESULT 34

US-09-616-651D-12/3

Sequence 12, Application US/0961651D

Patent No. 6410917

GENERAL INFORMATION:

APPLICANT: Farmer, Andrew

TITLE OF INVENTION: Recombinant Eucalyptus Globulus for Producing

TITLE OF INVENTION: Expression Vectors and Compositions for Use in Producing

TITLE OF INVENTION: The Same

FILE REFERENCE: SEQ ID NOS: 12

CURRENT APPLICATION NUMBER: 09/0961651D

CURRENT FILING DATE: 09-07-14

PRIOR APPLICATION NUMBER: 09/356,011

PRIOR FILING DATE: 09-07-14

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Pasteraq for Windows Version 4.0

SEQ ID NO 12

LENGTH: 34

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: primer

US-09-616-651D-12

Copy Match: 42.0%, Score 12.6, DP 4, Length 34

Best Local Similarity: 66.7%, Start No. 6, End No. 11

Mismatches: 19, Conservative: 0, Mismatched: 6, Indels: 0, Gaps: 0

4 AACATACCAAGGACCAATGATTA 30

30 AACATACCAAGGACCAATGATTA 4

RESULT 35

REFERENCE/INVENT NUMBER: 61547-80438005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (907) 841 3000
 TELEFAX: (907) 822-6944
 TELEX: 6714627000
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30
 TYPE: Nucleic acid
 STRANDEDNESS: Double-stranded
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-011-42337

Query Match 42.0% Score 12.6% DB 4 Length 30
 Best Local Similarity 78.9% Pred. No. 6.9e+03
 Matches 15 Conservative 0 Mismatches 4 Indels 0 Gaps 0

CV 11 ACCAAGCATATTACCA 29
 DB 2 AATAGAGAACACCAAGAA 20

RESULT 10
 US-08-544-381B-13/C
 Sequence 15: Application US/08-4418P
 Patent No. 6327890
 GENERAL INFORMATION:
 APPLICANT: Cronin, Maureen T.
 APPLICANT: Mayala, Charles Guillel
 APPLICANT: Hubbell, Emil A.
 APPLICANT: Chee, Mark
 APPLICANT: Fokle, Stephen P. A.
 APPLICANT: Huang, Xiaohua C.
 APPLICANT: Lipschutz, Robert J.
 APPLICANT: Lobban, Peter E.
 APPLICANT: Morrison, Macdonald S.
 APPLICANT: Sheldon, Edward L.
 TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
 TITLE OF INVENTION: Detecting Cystic Fibrosis
 NUMBER OF SEQUENCES: 290
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Federal Square Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/09-144,748
 FILING DATE: 18 OCT 1995
 CLASSIFICATION: 415
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/710,521
 FILING DATE: 02 AUG 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/094,113
 FILING DATE: 26 OCT 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 05/06784,064
 FILING DATE: 02 AUG 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 02/091,432,312
 FILING DATE: 26 OCT 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebeschuetz, Joe
 REGISTRATION NUMBER: 37,503

REFERENCE/INVENT NUMBER: 61547-80438005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-576-0200
 TELEFAX: 415-576-0300
 TELEX: 6714627000
 INFORMATION FOR SEQ ID NO: 153:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (oligonucleotide)
 US-08-544-381B-153

Query Match 42.0% Score 12.6% DB 4 Length 31
 Best Local Similarity 78.9% Pred. No. 6.9e+03
 Matches 15 Conservative 0 Mismatches 4 Indels 0 Gaps 0

CV 4 AGAGAGACAGAGAGATTT 22
 DB 29 AGAGAGACAGAGAGATTT 10

RESULT 31
 US-08-169-715-14/C
 Sequence 14: Application US/08169715
 Patent No. 6300056
 GENERAL INFORMATION:
 APPLICANT: Irvine, Bruce D.
 APPLICANT: Horn, Thomas
 APPLICANT: Chang, Chu-An
 TITLE OF INVENTION: HIV PROBES FOR USE IN SELECTIN-BASE
 TITLE OF INVENTION: CANCER HYBRIDIZATION ASSAYS
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 545 Middlefield Road, Suite 200
 CITY: Menlo Park
 STATE: California
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/169,715
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/913,693
 FILING DATE: 18-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Montoy, Gladys H.
 REGISTRATION NUMBER: 32,430
 REFERENCE/INVENT NUMBER: 08/09-70150,00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-613-5600
 TELEFAX: 415-327-2951
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-169-715-14

Query Match 42.0% Score 12.6% DB 4 Length 33
 Best Local Similarity 60.0% Pred. No. 6.9e+03
 Matches 15 Conservative 3 Mismatches 7 Indels 0 Gaps 0

CV 2 GCAAGAGACAGAGAGATTA 26

Material	Quantity	Unit	Value	Total
4	1000	kg	1000.00	1000.00
28	1000	kg	1000.00	1000.00

```

1 RESULT 27
2 US 03:11:573 2/5
3 September 27, Application US/041107
4 Patent No. 2004011073
5 GENERAL INFORMATION
6 APPLICANT: Kellough, Jill A.
7 APPLICANT: Kellough, Richard R.
8 TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROTOPHAGIC
9 TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROTOPHAGIC
10 NUMBER OF SEQUENCES: 17
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Dehlinger & Associates
13 STREET: 350 North 13th Avenue, Suite 200
14 CITY: Palo Alto
15 STATE: CA
16 COUNTRY: USA
17 ZIP: 94306
18 COMPUTER READABLE FORM:
19 MEDICAL FIELD: Disease
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: DOS
22 SOFTWARE: FASTSEQ for Windows Version 2.0
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/03/111,573
25 FILING DATE:
26 CLASSIFICATION:
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US/04/592,936
29 FILING DATE: 29-JAN-1994
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Evans, Susan T.
32 REGISTRATION NUMBER: 38,443
33 REFERENCE/SEQUENCE NUMBER: 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,
```

[illegible]

RESULT 29
 US 09 011 2230 7
 Sequence 7 Application 001030010230
 Patent No. 6255048
 GENERAL INFORMATION:
 APPLICANT: HOSOI, Shigeru
 KOLIMA, Makiko
 KADOGUCHI, Sachiko
 TITLE OF INVENTION: HIGH TEMPERATURE FIBERGLASS ADSORB
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PILLSBURY, MADISON & SUTRO
 31000 1100 NEW YORK AVENUE, N.Y.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: JIFFY Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #: 25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-011-2230
 FILING DATE: 09-Feb-1998
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul E. White, Jr.
 REGISTRATION NUMBER: 32,011

```

SOFTWARE: Word for Windows Version 2.0 Imported to 32 ASCII file
CURRENT APPLICATION DATA: US/09/890-363-3
APPLICATION NUMBER: 09/071,618
FILING DATE: 10-Aug-2000
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: US/09/487,716
FILING DATE: 19-Jan-2000
APPLICATION NUMBER: 09/071,618
FILING DATE: May 1, 1998
APPLICATION NUMBER: 09/071,739
FILING DATE: May 1, 1998
APPLICATION NUMBER: 09/022,180
FILING DATE: September 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 31,883
REFERENCE/AGENT NUMBER: 01/016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 372 3 562553
TELEFAX: 972 3 562554
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22
US-09-890-363-3
Query Match: 43.0% Score: 12.6 DB: 12 Length: 26
Best Local Similarity: 43.0% Freq: No. 8 Bases: 2
Matches: 18 Conservative: 0 Mismatches: 8 Indels: 0 Gaps: 0
QY 9 AACGACAAAGACTATGAG 27
DB 27 ACTCGACAAACTATGAG 9
RESULT 25
US-08-592-936R 2/c
Sequence 12, Application US/08/592936R
Patent No. 5781394
GENERAL INFORMATION:
APPLICANT: Bestwick, Richard K.
TITLE OF INVENTION: PLANT ISSUE / STAGE SPECIFIC PROMOTERS FOR
TITLE OF INVENTION: REGULATION EXPRESSION OF TRANSGENES IN PLANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennington & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,936R
FILING DATE: 29-JAN-1996
CLASSIFICATION: 600
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/AGENT NUMBER: 4257-0015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
US-08-592-936B 2

```

```

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: RANDOM primer
US-08-592-936B 2
Query Match: 43.0% Score: 12.6 DB: 12 Length: 30
Best Local Similarity: 43.0% Freq: No. 8 Bases: 2
Matches: 18 Conservative: 0 Mismatches: 8 Indels: 0 Gaps: 0
QY 4 AACGACAAAGACTATGAG 30
DB 28 MAAAAAAGAAAGCTATGAGCT 2
RESULT 26
US-08-788-928A 12/c
Sequence 12, Application US/08/78928A
Patent No. 5781394
GENERAL INFORMATION:
APPLICANT: Bestwick, Richard K.
TITLE OF INVENTION: FASTSEQ FOR WINDOWS VERSION 2.0
TITLE OF INVENTION: TRANSGENES IN PLANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennington & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,928A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 600
TITLE APPLICATION DATA:
APPLICATION NUMBER: US/08/792,936
FILING DATE: 29-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/AGENT NUMBER: 4257-0015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: RANDOM primer
US-08-788-928A 12
Query Match: 43.0% Score: 12.6 DB: 12 Length: 30
Best Local Similarity: 43.0% Freq: No. 8 Bases: 2
Matches: 18 Conservative: 0 Mismatches: 8 Indels: 0 Gaps: 0

```

FILING DATE: 10 JUNE 1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/030,408
 FILING DATE: 11-JUNE-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: BARRY J. SWANSON
 REGISTRATION NUMBER: 31,215
 REFERENCE/AGENT NUMBER: N/A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 793-3232
 TELEFAX: (202) 793-3232
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-867-421-10

Query Match: 42.7%, Score 12.5, DB 4, Length 30,
 Best Local Similarity: 66.7%, From DB: 50.0%,
 Matches: 16, Conservative: 1, Mismatches: 7, Gaps: 0,

CY 6 GAGATACGACATGATACAGCA 25
 DB 6 GAGGATACGACATGATACAGCA 25

RESULT 22
 US-09-514-247A-2/c
 Sequence 22, Application US/0904547A
 Patent No. 6363161
 GENERAL INFORMATION:
 APPLICANT: TANIUCHI, TOMOYASU
 APPLICANT: MIZUKAWA, JUNKO
 TITLE OF INVENTION: METHOD FOR IDENTIFYING A SPECIFIC ANTIBODY FOR ANTIBIOTIC TREATMENT
 FILE REFERENCE: TANIUCHI-6
 CURRENT APPLICATION NUMBER: US/01014,247A
 CURRENT FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: 07/030,408
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 07/014,111
 PRIOR FILING DATE: 1997-09-27
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 2
 LENGTH: 35
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Artificially synthesized protein sequence
 US-09-514-247A-2

Query Match: 42.7%, Score 12.5, DB 1, Length 35,
 Best Local Similarity: 70.6%, From DB: 50.0%,
 Matches: 17, Conservative: 2, Mismatches: 7, Gaps: 0,

CY 7 AACATGATATATATATATATATAT 40
 DB 35 AAGAGCTGAGGACATGATGATATAT 12

RESULT 23
 US-09-260-039B-22/c
 Sequence 22, Application US/0906039B
 Patent No. 6349344
 GENERAL INFORMATION:
 APPLICANT: MAY, AVAL Hershkowitz et al.
 TITLE OF INVENTION: GENETICALLY MODIFIED CELLS AND METHODS FOR
 EXPANDING RECOMBINANT HEPATINASE
 AND METHODS OF PURIFYING SAME
 NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mark M. Friedman, c/o Attilio Paulina
 STREET: 1000 Jefferson Davis Highway, Suite 207
 CITY: Arlington
 STATE: Virginia
 COUNTRY: United States of America
 ZIP: 22202
 COMPUTER FILED FORM:
 MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
 COMPUTER: Windows 95, 31Mbyte-8607X
 OPERATING SYSTEM: MS DOS version 6.2,
 Windows version 3.11
 CONTACT: Mark M. Friedman, c/o Attilio Paulina
 an ASCII file
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/260,039B
 FILING DATE: 02-MAR-1999
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/011,918
 FILING DATE: May 1, 1998
 APPLICATION NUMBER: 01/071,739
 FILING DATE: May 1, 1998
 APPLICATION NUMBER: 09/022,180
 FILING DATE: September 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Friedman, Mark M.
 REGISTRATION NUMBER: 33,983
 REFERENCE/AGENT NUMBER: 310,716
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-5625553
 TELEFAX: 703-5625554
 TELEX: <unknown>
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-260-039B-22

Query Match: 42.7%, Score 12.4, Length 29,
 Best Local Similarity: 76.7%, From DB: 6.8%,
 Matches: 15, Conservative: 0, Mismatches: 3, Gaps: 0,

CY 9 AACCAAGACACTACCG 27
 DB 27 ACTCCAGACACTACCG 9

RESULT 24
 US-09-635-923-22/c
 Sequence 22, Application US/09063923
 Patent No. 6362409
 GENERAL INFORMATION:
 APPLICANT: MAY, AVAL Hershkowitz et al.
 TITLE OF INVENTION: GENETICALLY MODIFIED CELLS AND METHODS FOR
 EXPANDING RECOMBINANT HEPATINASE
 AND METHODS OF PURIFYING SAME
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
 STREET: 2001 Jefferson Davis Highway, Suite 207
 CITY: Arlington
 STATE: Virginia
 COUNTRY: United States of America
 ZIP: 22202
 COMPUTER FILED FORM:
 MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
 COMPUTER: PC
 OPERATING SYSTEM: MS DOS version 6.2,
 Windows version 3.11

COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US06/194,798A
FILING DATE: 02-FEBRUARY-1996
CLASSIFICATION: 36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,006
FILING DATE: 10-FEBRUARY-1994
CLASSIFICATION: 36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/736,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,210
REFERENCE/AGENT NUMBER: NEX/76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 793-3333
TELEFAX: (603) 792-3413
INFORMATION PER SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-184-708A-10

Query Match: 42.7% Score 12.9 DB 1 Length 30
Best Local Similarity: 40.7% Prod No 576421
Matches: 16; Conservative: 1; Mismatches: 7; Indels: 0; Gaps: 0

CY 6 GAGACACCAAGACACTACAGCA 29
DB 6 GAGCCTAACAGACACAGCAGCA 29

RESULT 20
US 06 535 4113
Sequence 9, Application US/05535443
Patent No. 5965551
GENERAL INFORMATION:
APPLICANT: Benoit, Patrick
APPLICANT: Denefle, Patrice
APPLICANT: Pericaudet, Michel
APPLICANT: Sautet, Sandrine
APPLICANT: Vigne, Emmanuelle
TITLE OF INVENTION: RECOMBINANT VIRUSES AND THEIR USE IN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: 500 Arcadia Road, 2043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09,697,243
FILING DATE: 07/09/1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/107,664/00442
FILING DATE: 15-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/05125
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie Y
REGISTRATION NUMBER: 38,619
REFERENCE/AGENT NUMBER: 07/032,005-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3804
INFORMATION PER SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Adeno virus 11b, 1120"
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-890-363-3

Query Match: 42.7% Score 12.8 DB 2 Length 30
Best Local Similarity: 40.7% Prod No 576421
Matches: 14; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0

CY 5 AGAGACCAAGACAGCA 20
DB 5 ACAGACCAAGACAGCA 20

RESULT 21
US 09 497 421-10
Sequence 10, Application US/09497421
Patent No. 6179557
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Jassie, Neboisa
APPLICANT: Tasset, Diane
TITLE OF INVENTION: HIGH AFFINITY MEANS OF ELAID
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR ANT
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Plentico Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09,667,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/179,095
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,912
FILING DATE: 29-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/073,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131

Db 30 ACAAAGCAAAAGCTACCTGCA 10

RESULT 16
US-09-071-101-6/c

Sequence 6, Affili: 1998-05-06
Patent No. 6013503

GENERAL INFORMATION:
APPLICANT: Lok, SI

APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: HUMAN FRAGMENT

NUMBER OF SEQUENCES: 11
CORRESPONDENT ADDRESS:
ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA

COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,101

CLASSIFICATION:
FILING DATE:
PRIORITY DATE: 1998-05-06

PRICE AFFILIATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Patrick, Guy F.
REGISTRATION NUMBER: 11,648

REFERENCE/DOCKET NUMBER: 11,648
TELEPHONE: 206-442-6673
TELEFAX: 206-442-6678

TELEX:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ZC11809

US-09-071-101-6

Query Match 42.7% Score 12.9; DB 3; Length 25;
Best Local Similarity 87.5%; Freq No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 12 CCAAGACACTACGAG 27

US-09-369-617-7/c

Sequence 7, Affili: 1998-05-06
Patent No. 612712

GENERAL INFORMATION:
APPLICANT: Lok, SI

APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: HUMAN FRAGMENT

NUMBER OF SEQUENCES: 11
CORRESPONDENT ADDRESS:
ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA

COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:

EARLIER FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 7
LENGTH: 25
TYPE: DNA
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ZC11809

US-09-369-617-7

Query Match 42.7% Score 12.9; DB 3; Length 25;
Best Local Similarity 87.5%; Freq No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 12 CCAAGACACTACGAG 27

US-09-369-617-7/c

Sequence 7, Affili: 1998-05-06
Patent No. 612712

GENERAL INFORMATION:
APPLICANT: Lok, SI

APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: HUMAN FRAGMENT

NUMBER OF SEQUENCES: 11
CORRESPONDENT ADDRESS:
ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA

COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

US-09-369-617-7

Query Match 42.7% Score 12.9; DB 3; Length 25;
Best Local Similarity 87.5%; Freq No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 12 CCAAGACACTACGAG 27

US-08-384-708A-10

Sequence 10, Application US/08384/08A
Patent No. 5639868

GENERAL INFORMATION:
APPLICANT: Gold, Larry

APPLICANT: Janjic, Nebojsa
TITLE OF INVENTION: HUMAN FRAGMENT

NUMBER OF SEQUENCES: 27
CORRESPONDENT ADDRESS:
ADDRESSEE: Swanson & Frateschun, Ltd. Co.

STREET: 641 E. Fredrick Avenue, Suite 200
CITY: Englewood
STATE: Colorado

COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

11 ACCAAGACATACCTA 2A
18 ATCAGACATACCTAC 1

RESULT 10

US-08-198-670A-12/C
Sequence 12, Application US/08198670A
Patent No. 5707926

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY

INVENTOR: GOLD, LARRY

TITLE OF INVENTION: METHOD FOR SELECTING NUCLEOTIDE SEQUENCES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSER: SWANSON & BRIDGEMAN, L.L.C.
STREET: 3400 S. FLORENCE AVE., SUITE 200
CITY: ENGLEWOOD
STATE: COLORADO
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 6.0 for windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/198,670A

FILING DATE: 22 FEBRUARY-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 14 OCTOBER-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,429

FILING DATE: 11 JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: 07/714,131

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ. ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-198-670A-12

Query Match 44.0% Score 12.3 DB 57 Length 37

Post local similarity 52.0% E-Value 1.1e-13

Matches 19, Conserved 10, Mismatches 8, Gaps 0

1 GGCAAGACATACCTA 26

28 GGCAAGACATACCTA 3

RESULT 11

PCT US/93 09695 12/C

Sequence 12, Application US/09198670A

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY M.

INVENTOR: BEUTEL, BRUCE

TITLE OF INVENTION: METHOD OF SELECTING NUCLEOTIDE SEQUENCES

TITLE OF INVENTION: THE BASIS OF STRUCTURE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSER: Beaton & Swanson, P.C.

STREET: 4582 South Uteer Street Parkway, #403

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80237

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 KB storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/09695

FILING DATE: 12-OCT-1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/540,093

FILING DATE: 14-OCTOBER-1992

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 850-9900

TELEFAX: (303) 850-9401

INFORMATION FOR SEQ. ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT US/93 09695 12

Query Match 44.0% Score 12.3 DB 57 Length 37

Post local similarity 52.0% E-Value 1.1e-13

Matches 19, Conserved 10, Mismatches 8, Gaps 0

1 GGCAAGACATACCTA 26

28 GGCAAGACATACCTA 3

RESULT 12

US-07-124-500B-8/C

Sequence 9, Application US/07/24500B

Patent No. 578294

GENERAL INFORMATION:

APPLICANT: Becker et al

TITLE OF INVENTION: REAGENT AND METHOD FOR IDENTIFYING AND EXTENDING THE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSER: MacLewicz & No. 57829415

STREET: One Liberty Place - 46th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM 1974

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/124,500B

THE

Matches	15	Conservative	0	Mistakes	4	2000
1	1	1	1	1	1	1
2	1	1	1	1	1	1
3	1	1	1	1	1	1
4	1	1	1	1	1	1
5	1	1	1	1	1	1
6	1	1	1	1	1	1
7	1	1	1	1	1	1
8	1	1	1	1	1	1
9	1	1	1	1	1	1
10	1	1	1	1	1	1
11	1	1	1	1	1	1
12	1	1	1	1	1	1
13	1	1	1	1	1	1
14	1	1	1	1	1	1
15	1	1	1	1	1	1
16	1	1	1	1	1	1
17	1	1	1	1	1	1
18	1	1	1	1	1	1
19	1	1	1	1	1	1
20	1	1	1	1	1	1
21	1	1	1	1	1	1
22	1	1	1	1	1	1
23	1	1	1	1	1	1
24	1	1	1	1	1	1
25	1	1	1	1	1	1
26	1	1	1	1	1	1
27	1	1	1	1	1	1
28	1	1	1	1	1	1
29	1	1	1	1	1	1
30	1	1	1	1	1	1
31	1	1	1	1	1	1
32	1	1	1	1	1	1
33	1	1	1	1	1	1
34	1	1	1	1	1	1
35	1	1	1	1	1	1
36	1	1	1	1	1	1
37	1	1	1	1	1	1
38	1	1	1	1	1	1
39	1	1	1	1	1	1
40	1	1	1	1	1	1
41	1	1	1	1	1	1
42	1	1	1	1	1	1
43	1	1	1	1	1	1
44	1	1	1	1	1	1
45	1	1	1	1	1	1
46	1	1	1	1	1	1
47	1	1	1	1	1	1
48	1	1	1	1	1	1
49	1	1	1	1	1	1
50	1	1	1	1	1	1
51	1	1	1	1	1	1
52	1	1	1	1	1	1
53	1	1	1	1	1	1
54	1	1	1	1	1	1
55	1	1	1	1	1	1
56	1	1	1	1	1	1
57	1	1	1	1	1	1
58	1	1	1	1	1	1
59	1	1	1	1	1	1
60	1	1	1	1	1	1
61	1	1	1	1	1	1
62	1	1	1	1	1	1
63	1	1	1	1	1	1
64	1	1	1	1	1	1
65	1	1	1	1	1	1
66	1	1	1	1	1	1
67	1	1	1	1	1	1
68	1	1	1	1	1	1
69	1	1	1	1	1	1
70	1	1	1	1	1	1
71	1	1	1	1		

Best local similarity 83.78; p

```

FILE REFERENCE: 1948/10042
CURRENT APPLICATION NUMBER: US-09-159-66/6
CURRENT FILING DATE: 1998-04-27
EARLIER FILING DATE: 1998-04-27
EARLIER APPLICATION NUMBER: 60/041,938
EARLIER FILING DATE: 1987-04-03
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 58
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FOR BLASTP
US-09-159-66

Query Match      46.0%  Score 13.8  DB 4  Length 20
Best Local Similarity 98.2%  Ident. No. 2,1e+03
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      4  AGAGAGCAGCAGAGACA 20
      |||||
DB      19  AGAGTCAGCAGAGACA 3

RESULT 4
US-09-159-66/6
Sequence 66, Application US-09-159-66/6
Patent No. 619706
GENERAL INFORMATION:
APPLICANT: NO: 619706berg, Leif T
APPLICANT: Andersen, Maria K
TITLE OF INVENTION: METHOD FOR ASSESSING IMMUNOLOGICAL STATUS AND
TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
FILE REFERENCE: 1948/10042
CURRENT APPLICATION NUMBER: US-09-159-66/6
CURRENT FILING DATE: 1998-04-27
EARLIER FILING DATE: 1997-04-27
EARLIER APPLICATION NUMBER: 60/041,938
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 66
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FOR BLASTP
US-09-159-66

Query Match      46.0%  Score 13.8  DB 4  Length 20
Best Local Similarity 98.2%  Ident. No. 2,1e+03
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      4  AGAGAGCAGCAGAGACA 20
      |||||
DB      19  AGAGTCAGCAGAGACA 3

RESULT 5
US-09-159-66/6
Sequence 66, Application US-09-159-66/6
Patent No. 625512
GENERAL INFORMATION:
APPLICANT: Tiedje, Mark A
APPLICANT: Mahawale, Gabriel
TITLE OF INVENTION: Segmentation of Hsp-Related Gene Cell Differentiation
TITLE OF INVENTION: Segmentation of Hsp-Related Gene Cell Differentiation
FILE REFERENCE: 60/040,332
CURRENT APPLICATION NUMBER: US-09-159-66/6
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/039,233
EARLIER FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: 60/039,233

```

```

EARLIER FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: FOR BLASTP
US-09-159-66

Query Match      46.0%  Score 13.8  DB 4  Length 20
Best Local Similarity 98.2%  Ident. No. 2,1e+03
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      3  AGAGTCAGCAGAGACA 19
      |||||
DB      3  AGAGTCAGCAGAGACA 19

RESULT 6
US-09-905-223-15
Sequence 15, Application US-09-905-223-15
Patent No. 622029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' Ends for C-ESTERON (HOLINS)
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESS: 101 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
E-MAIL: j223@ucsd.edu
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-905-223-15
FILING DATE:
CLASSIFICATION: 536
APPLICANT/AGENT INFORMATION:
NAME: Israelson, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DEPOSIT NUMBER:
TELEPHONE/TELEFAX INFORMATION:
TELEPHONE: (619) 235-0176
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Other nucleic acid
US-09-905-223-15

Query Match      45.3%  Score 13.6  DB 4  Length 29
Best Local Similarity 98.0%  Ident. No. 2,1e+03
Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0

CY      5  AGAGTCAGCAGAGACA 24
      |||||
DB      6  AGAGTCAGCAGAGACA 25

RESULT 7
US-09-247-155-15

```




RESULT 40

AA33076 standard; DNA; 29 BP.

XX AA33076;

XX 17 JUN-1999 (first entry)

XX Oligodeoxynucleotide PCR primer SEQ ID NO:15.

XX Human, secreted protein; EST; expressed sequence tag; diagnosis;

XX (oncogenic gene therapy, chemokine binding, signal peptide);

XX (differentiation, hematopoietic, cytokine activity, cell proliferation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

XX (differentiation, hematopoietic, cytokine activity, tissue growth regulation);

Query Match 45.3%; Score 13.6; DP 20; Length 29;

Best local similarity 90.0%; Prod. No. 1.00.04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 5 AGAGACACCAAGACACTAC 24

DB 5 AGAGTCACGAGAGACTAC 25

Search completed: July 21, 2003, 14:05:51

Job time: 119.538 secs

Query Match 45.3% Score 13.6 DB 20 Length 29
 Best Loc 1 Similarity 80.0% Seed No 1 W 4
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

5 AGAGACACCAAGACTAC 24
 |||||
 6 AGAGTCACGAGAGACTAC 25

RESULT 18

AAAX1770
 ID AAXS1770 standard; DNA; 29 BP.

XX AAXS1770;
 XX

XX 22 JUN 1999 (first entry)
 XX

DE Oligodeoxynucleotide primer for EST sequence.

XX Human, secreted protein, EST, expressed sequence tag, diagnosis; PCR;
 XX forensic, gene therapy, chromosome mapping, signal peptide;
 XX differential gene therapy, chromosome mapping, cell proliferation;
 XX differential gene therapy, chromosome mapping, cell growth regulation;
 XX reproductive hormone regulation; chemokine; chemokine; chemokine;
 XX reproductive hormone regulation; chemokine; chemokine; chemokine;
 XX reproductive hormone regulation; chemokine; chemokine; chemokine;
 XX

XX Synthetic.
 XX Homo sapiens.

XX W09906552-A2.
 XX

XX 11 FEB 1999.
 XX

XX 31 JUL 1998; 98WD 1801236.
 XX

XX 01 AUG 1997; 97US 0905223.
 XX

XX (BEST) GENSET.
 XX

XX Doclet A, Dumas Milne Edwards J, Lacroix P.
 XX

XX WFI: 1999-15700713.
 XX

XX Now isolated from derived from human cells used to develop products
 XX which may have an effect on human health, regulatory, hematopoietic
 XX regulating, anti-inflammatory or tumor inhibition activity

XX Example 27, Page 41, 41pp; English.

XX Example 27, Page 41, 41pp; English.

XX AAXS1770 is present in expressed sequence tag (EST) for
 XX human secreted protein, and encodes the protein given in AAXS1770
 XX AAXS1770, respectively, the protein given in AAXS1770
 XX and an N-terminal fragment of a secreted protein. The signal peptide
 XX sequences can be used for producing secreted human gene products. They
 XX can also be used to develop a gene for diagnosis and therapy. The
 XX proteins obtained may have cytokine activity, cell
 XX proliferation/differentiation activity, hematopoietic regulating
 XX activity, tissue growth regulation activity, reproductive hormone
 XX regulating activity, chemokine/chemokine activity, hematopoietic and
 XX thrombolytic activity, secreted signal peptide, and inflammatory
 XX activity, tumor inhibition activity or other activities. The products
 XX can be used in forensic, gene therapy and chromosome mapping procedures.
 XX The sequences can also be used for obtaining corresponding promoter
 XX sequences, the nucleotide sequence of a polyepitope can be used for
 XX detecting extracellular secretion of a polypeptide on the insertion of a
 XX polypeptide in a membrane, or inserting a polypeptide into a cell.
 XX This sequence is a second strand cDNA synthesis primer used in a cell
 XX for isolating the 5' ESTs of the genes encoding the human secreted
 XX proteins of the invention.

XX Sequence 29 BF; 10 A; 8 C; 9 G; 2 T; 0 other;
 XX

Query Match 45.3% Score 13.6 DB 20 Length 29;

Best Loc 1 Similarity 80.0% Seed No 1 W 4
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

5 AGAGACACCAAGACTAC 24
 |||||
 6 AGAGTCACGAGAGACTAC 25

RESULT 39

AAAX1362
 ID AAX41362 standard; DNA; 29 BP.

XX AAX41362;
 XX

XX 22 JUN 1999 (first entry)
 XX

DE Oligodeoxynucleotide primer, SEQ ID NO: 15 from W09906554

XX Human, secreted protein, EST, expressed sequence tag, diagnosis;
 XX forensic, gene therapy, chromosome mapping, signal peptide;
 XX differential gene therapy, chromosome mapping, cell proliferation;
 XX differential gene therapy, chromosome mapping, cell growth regulation;
 XX reproductive hormone regulation; chemokine; chemokine; chemokine;
 XX reproductive hormone regulation; chemokine; chemokine; chemokine;
 XX reproductive hormone regulation; chemokine; chemokine; chemokine;
 XX

XX Homo sapiens.
 XX

XX W09906551-A2.
 XX

XX 11 FEB 1999.
 XX

XX 31 JUL 1998; 98WD 1801237.
 XX

XX 01 AUG 1997; 97US 0905051.
 XX

XX (BEST) GENSET.
 XX

XX Doclet A, Dumas Milne Edwards J, Lacroix P.
 XX

XX WFI: 1999-15700713.
 XX

XX Now isolated from derived from human cells used to develop products
 XX which may have an effect on human health, regulatory, hematopoietic
 XX regulating, anti-inflammatory or tumor inhibition activity

XX Example 27, Page 45, 41pp; English.

XX Example 27, Page 45, 41pp; English.

XX The patent related to sequence of 5' ESTs derived from AAXS1770
 XX encoding secreted protein, and encodes the protein given in AAXS1770
 XX AAXS1770, respectively, the protein given in AAXS1770
 XX and an N-terminal fragment of a secreted protein. The signal peptide
 XX sequences can be used for producing secreted human gene products. They
 XX can also be used to develop a gene for diagnosis and therapy. The
 XX proteins obtained may have cytokine activity, cell
 XX proliferation/differentiation activity, hematopoietic regulating
 XX activity, tissue growth regulation activity, chemokine/chemokine
 XX activity, thrombolytic activity, secreted signal peptide, and inflammatory
 XX activity, tumor inhibition activity or other activities. The products
 XX can be used in forensic, gene therapy and chromosome mapping procedures.
 XX The sequences can also be used for obtaining corresponding promoter
 XX sequences, the nucleotide sequence of a polyepitope can be used for
 XX detecting extracellular secretion of a polypeptide on the insertion of a
 XX polypeptide in a membrane, or inserting a polypeptide into a cell.
 XX This sequence is a second strand cDNA synthesis primer used in a cell
 XX for isolating the 5' ESTs of the genes encoding the human secreted
 XX proteins of the invention.

XX Sequence 29 BF; 10 A; 8 C; 9 G; 2 T; 0 other;
 XX

Query Match 45.3% Score 13.6 DB 20 Length 29;

Best Loc 1 Similarity 80.0% Seed No 1 W 4
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

5 AGAGACACCAAGACTAC 24
 |||||
 6 AGAGTCACGAGAGACTAC 25

WP1: 1999-147470/20
 XX
 XX Extended clones encoding secreted proteins
 PT
 XX Example 27, Page 113, 117ff, English.
 PS
 XX
 CC This invention relates to novel nucleic acid sequences of extended clones
 CC (see AAX51442) which encode human secreted proteins (see
 CC AAX51442) and which have cytostatic, chemotherapeutic and cytotoxic
 CC activity. The extended clones can be used to express secreted proteins
 CC or parts of them or to obtain antibodies capable of binding to the
 CC secreted proteins. They may also be used in diagnostic, therapeutic,
 CC gene therapy, and in vaccine coding procedures. These also include design
 CC of expression vectors and secretion vectors. This sequence represents
 CC a PCR primer used in the method of the invention.
 XX
 SQ Sequence 29 BP, 10 A, 8 C, 9 G, 2 T, 0 other:
 Query March 45 38 Score 13.6, DP 20, Length 29,
 Best local similarity 40.08, Pred. No. 1.9e+04,
 Matches 16, Conservation of Mismatches 4, Indels 0, Gaps 0,
 QY 5 AGAGTACGAGAGAGACTAC 24
 ID AAX51442 standard, DNA, 29 BP.
 AC AAX51442:
 XX
 XX AAX51442:
 DE 13-SEP 1999 (first entry)
 XX
 DE PCR primer for extended secreted protein coding sequences.
 XX
 KW Secreted protein; human; cytokine; cellular proliferation; cell movement;
 KW cellular differentiation; immune system regulator; anti-inflammatory;
 KW haematopoietic regulation; tissue growth regulator; tumour inhibitor;
 KW reproductive hormone regulation; chemotaxis; chemokinesis; gene therapy;
 KW genetic disease; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PA WO99031236 A2
 PD 24-JUN 1999.
 XX
 PF 17-DEC 1998; 98MO 1802122.
 XX
 FF 10-AUG-1998; 98US 0066116.
 FR 17-DEC-1997; 97US 0069957.
 FR 09-FEB-1998; 98US 0074121.
 FR 13-APR 1998; 98US 0081583.
 XX
 PA (GEST) GENSET.
 XX
 PI Bouquollet L, Duclert A, Dumas Milne Edwards J;
 XX
 XX WP1: 1999-147470/20.
 PT How isolated human secreted proteins
 PT
 XX Example 27, Page 113, 117ff, English.
 XX
 CC This sequence represents a PCR primer used in the isolation of the
 CC extended human secreted protein coding sequences (see the invention). The
 CC extended clones can be used to express secreted proteins or parts of a variety of
 CC human secreted proteins. The secreted proteins may act as cytokines or may
 CC affect cellular proliferation and differentiation. They may act as immune
 CC system regulators, haematopoietic regulators, tissue growth regulators,

XX regulators of reproductive hormone or cell movement of bone
 CC chemokine/chemotactic factor/ligand, anti-inflammatory or tumour
 CC inhibition activity. The DNAs can be used in forensic procedures to
 CC identify individuals or in diagnostic procedures to identify individuals
 CC having genetic disease or to obtain antibodies capable of binding to the
 CC secreted proteins. They may also be used in diagnostic, therapeutic,
 CC gene therapy, and in vaccine coding procedures. This sequence represents
 CC a PCR primer used in the method of the invention.
 XX
 SQ Sequence 33 BP, 10 A, 8 C, 9 G, 2 T, 0 other:
 Query March 45 38 Score 13.6, DP 20, Length 29,
 Best local similarity 40.08, Pred. No. 1.9e+04,
 Matches 16, Conservation of Mismatches 4, Indels 0, Gaps 0,
 QY 5 AGAGTACGAGAGAGACTAC 24
 ID AAX51442 standard, DNA, 29 BP.
 AC AAX51442:
 XX
 XX AAX51442:
 DE 21-JUN-1999 (first entry)
 XX
 DE PCR primer for 5' FET sequence.
 XX
 KW Human; secreted protein; EST; expressed sequence; any diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine; cellular proliferation;
 KW differentiation; haematopoietic regulation; tissue growth regulator;
 KW reproductive hormone regulation; chemotaxis; chemokinesis; haematopoietic
 KW chemotaxis; cell differentiation; gene therapy; tumour inhibitor; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98MO 1801231.
 XX
 FF 03-AUG-1997; 97US 0060729.
 XX
 PA (GEST) GENSET.
 XX
 PI Duclert A, Dumas Milne Edwards J, Lacroix B;
 XX
 XX WP1: 1999-153706/13.
 PT New nucleic acids encoding human secreted proteins obtained from
 PT cDNA libraries derived from testis, ovary, uterus and spleen tissue
 XX
 XX Example 27, Page 143, 147ff, English.
 XX
 CC AAX51459 to AAX51601 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAX51459 to
 CC AAX51601, respectively. The proteins given represent the original protein
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for predicting secreted human gene products. They
 CC can also be used to develop probes for diagnostic and therapy. The
 CC proteins obtained by these genes may be used for diagnostic and therapy. The
 CC expression/differentiation activity, haematopoietic regulation,
 CC activity, tissue growth regulation activity, cell movement, tumour
 CC inhibiting activity, chemotaxis/chemotactic activity, haematopoietic and
 CC haematopoietic activity, cytokine/ligand activity, anti-inflammatory
 CC activity, gene inhibition activity, cell differentiation, the proteins
 CC can be used in forensic, gene therapy, and in vaccine mapping procedures.
 CC The sequence can also be used for the isolation of secreted proteins

CC treatment regimen. Adverse events in an early trial can be evaluated to
 CC identify polymorphic patterns so that the adverse results can be
 CC correlated with a sub-population of the test population, permitting
 CC exclusion of such sub-populations from the treatment group. Identifying
 CC drugs can be approved for use in the appropriate population, thereby
 CC decreasing the number of patients required for a clinical trial, which
 CC in turn decreases the duration and cost of such trials. Sequences
 CC AAH48252 and 48267 represent PCR primers used in an exemplification of
 CC the invention to amplify short fragments of the human angiotensinogen
 CC gene coding region (AAH48252 A78327) for sequence determination.

CC Sequence 20 BP: 1 A; 6 C; 5 G; 8 T; 0 other;

Query Match 46.08; Score 13.8; DB 21; Length 20;

Best local similarity 24.24; Pos: 1, 5, 7, 8, 9;

Matches 1; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC 4 AAACAGACAGACAGACA 20

19 AAACAGACAGACAGACA 3

RESULT 25

AAZ600/0 standard; cDNA; 40 BP.

AAZ60070;

25 APR 2000 (first entry)

PCR primer for osteoprotegerin amplification.

PCR primer; human, osteoprotegerin, OPG, CD34+ cell, ss,

mesenchymal stem cell, osteoblast precursor, human fetal bone cell

Homo sapiens.

W0604565.A2

16 DEC 1999.

08 JUN 1999; 99WD-US12847.

04-JUN-1999; 99US-009441.

04-SEP-1998; 98US-0099233.

(GenR) GENRIS THERAPEUTICS INC.

Thiede MA, Mbalaviele G;

WPI; 99-11447311.

Producing osteoclasts in vitro.

Example 6, Page 17, 48PP, English.

This sequence represents a PCR primer used in osteoprotegerin

amplification from human cells derived from osteoblasts and osteoclast

lineages. The primer is used in a method for producing osteoclasts in

vitro. The method comprises culturing mesenchymal stem cells with

osteoblasts. The human mesenchymal stem cells are used to induce the

differentiation of human CD34+ cells into osteoclast cells. Osteoclasts

are not strictly isolated but rather the cell culture and their

fragility and tendency to adhere to other bone cells. The CD34+ cells can

be maintained and utilized as a source of osteoclasts, allowing efficient

in vitro differentiation of bone.

CC 4 AAACAGACAGACAGACA 24

19 AAACAGACAGACAGACA 19

RESULT 26

AAH40390 standard; cDNA, 24 BP.

AAH40390;

14-AUG-2001 (first entry)

SNF specific lower PCR primer SEQ ID 3166.

Single nucleotide polymorphism (SNP), single nucleotide primer extension

SNPE, genotyping, agammaglobulinemia, diabetes mellitus, cancer,

leuk, myeloid syndrome, muscular dystrophy, familial hypercholesterolemia,

polycystic kidney disease, osteogenesis imperfecta, autoimmune disease,

acute intermittent porphyria, rheumatoid arthritis, multiple sclerosis,

diabetes, fibrodysplasia ossificans, frequency polymorphic primer ss

Homo sapiens.

W06012462.A2.

26-APR-2001.

15-OUT-2000; 2000W01482436.

15-SEP-1999; 99US-0160096.

PCR primer for SNPE.

Picoult-Newburg L, Pohl M;

WPI; 2001-240900/30.

New genotyping oligonucleotide, useful for detecting the presence,

absence or identity of single polymorphic polymorphisms in a nucleic

acid sample.

Claim 1; Page 001 5PP; English.

Sequences AAH37205 - AAH3994 represent PCR primers, single nucleotide

primer extension (SNPE) primers, and the sequences of regions flanking

sites of single nucleotide polymorphisms SNPs. The present invention

includes kits for determining the presence or absence of a SNP, using the

oligonucleotides of the invention. The PCR primers are used to amplify a

SNP flanking sequence, the SNP primer is used as a genotyping primer

The oligonucleotides are used for genotyping a nucleic acid sample by

performing a single-nucleotide primer extension reaction. The

oligonucleotides are useful for determining the presence, absence or

identity of a SNP and for genotyping nucleic acid samples, for example,

assess by association analysis the genotype of an individual or group of

individuals, having a pathological phenotype trait suspected of being

caused by one or more SNPs. Phenotypic traits include diseases such

as agammaglobulinemia, diabetes mellitus, cancer, myeloid syndrome,

leukemia, familial hypercholesterolemia, polycystic kidney disease,

osteogenesis imperfecta, autoimmune disease, acute intermittent porphyria,

rheumatoid arthritis, multiple sclerosis, fibrodysplasia ossificans,

diabetes mellitus, frequency polymorphic primer ss

inflammation, cancer, nervous system diseases and information by pathogen

antigenism. The method is also useful to identify lower-lipid and

paternity analysis. The present sequence represents a PCR primer specific

for a human SNF containing DNA sequence.

Sequence 24 BP: 4 A; 6 C; 3 G; 7 T; 0 other;

Query Match 46.08; Score 13.8; DB 21; Length 20;

Best local similarity 24.24; Pos: 1, 5, 7, 8, 9;

Matches 1; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches: 18; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;

CY 3 CAAAGAGAACCAAGACACTACC 25
 DB 2 CCAAGAGAACCAAGACACTACC 24

RESULT 7

AAFS4411

ID AAF54411 standard; DNA; 24 BP

XX
 AC AAF54411;

XX
 02 APR-2001 (first entry)

DE DNA encoding protein of the invention #82.

KW Secreted; transmembrane; gene therapy; ss.

XX
 OS Unidentified.

XX
 MO2000/0961 A1.

XX
 26 DEC-2000.

XX
 18 FEB-2000; 2000MO US04342.

XX
 24 JUN-1999; 99US-0141017.

XX
 20 JUL-1999; 99US-0144798.

XX
 26 JUL-1999; 99US-0145698.

XX
 01 SEP-1999; 99US-0320111.

XX
 24 OCT-1999; 99US-0162506.

XX
 30 NOV-1999; 99MO US48413.

XX
 02 DEC-1999; 99MO US48551.

XX
 16 DEC-1999; 99MO US48951.

XX
 05 JAN-2000; 2000MO US49113.

XX
 06 JAN-2000; 2000MO US49113.

XX
 (GENT) GENENTECH INC.

XX
 Baker RP, Portierot D, Desnoyers L, Egan G, Fortana R, Fong C,

XX
 Gao W, Gubler A, Gubler R, Gubler R, Gubler R, Gubler R,

XX
 Pan D, Paoletti M, Roy MA, Smith V, Stewart TA, Thomas D,

XX
 Watanabe Y, Williams RW, Williams RW.

XX
 WI, 2001 01133/08.

XX
 Secreted and transmembrane proteins and nucleic acids designed for

XX
 useful in hybridization, PCR, in vitro, in vivo and gene therapy

XX
 therapy

XX
 Claim 2; Fig 16; 787pp; English

XX
 The present invention relates to secreted and transmembrane proteins.

XX
 These proteins and the DNA encoding them may be used as hybridization

XX
 probes, in diagnosis and gene mapping and in the generation of

XX
 anti-sense RNA and DNA. They may also be used to generate either

XX
 transgenic animals or knockout animals which are in turn useful for

XX
 development and screening of therapeutically useful reagents.

XX
 The nucleic acids may also be used in gene therapy.

XX
 Sequence 24 BP; 7 A; 12 G; 2 C; 3 T; 0 other;

XX
 Query Match 50.0%; Score 15; DB 24; Length 24;

XX
 Best Local Similarity 78.7%; Pred. No. Errors;

XX
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX
 3 CAAAGAGAACCAAGACACTACC 25

XX
 2 CCAAGAGAACCAAGACACTACC 24

XX
 RESULT 8

AAW91351

ID AAX91351 standard; DNA; 23 BP.

XX
 AAX91351;

XX
 24 SEP-1999 (first entry)

XX
 Primer for RT-PCR analysis of T. gondii immunogenic protein DNA.

XX
 Immunogenic protein; Toxoplasma gondii; gene; shedding; cell;

XX
 T. gondii; infection; culture; Toxoplasma gondii; cell; shedding; cell;

XX
 Toxoplasma gondii; RT-PCR primer; ss.

XX
 OS Synthetic.

XX
 Toxoplasma gondii.

XX
 MO9932633-A1.

XX
 01 JUL-1999.

XX
 18 DEC 1998; 99MO US27137.

XX
 19 DEC-1997; 97US-0394825.

XX
 (HESK-) HESKA CORP.

XX
 Lutz SB, Milhausen MJ, Ng RK;

XX
 WPI; 1999-418930/35.

XX
 Example 2; Page 68; 36pp; English.

XX
 The invention provides isolated Toxoplasma gondii nucleic acids that

XX
 encode immunogenic polypeptides. The T. gondii nucleic acid molecules

XX
 immunogenic proteins and are utilized to the invention can be used to

XX
 inhibit T. gondii oocyst shedding in a rat due to infection with

XX
 T. gondii. They can be used for preventing T. gondii infection and for

XX
 detecting T. gondii infection. The invention can be used to

XX
 detect parasite cysts in feces, and from which oocysts can be

XX
 detected. Such as T. gondii oocysts and T. gondii cysts.

XX
 Sequences AAX91276-335 primers used in RT-PCR analysis of nucleic acid

XX
 sequences encoding immunogenic T. gondii proteins.

XX
 Sequence 23 BP; 7 A; 7 G; 6 C; 1 T; 0 other;

XX
 Query Match 48.7%; Score 14.6; DB 26; Length 24;

XX
 Best Local Similarity 81.0%; Pred. No. Errors;

XX
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX
 7 AAGAGAGAACCAAGACACTACC 27

XX
 1 AAGAGAGAACCAAGACACTACC 21

XX
 RESULT 9

XX
 AAS42674

XX
 ID AAS42674 standard; DNA; 23 BP.

XX
 AAS42674;

XX
 17 DEC-2001 (first entry)

XX
 T. gondii immunogenic protein PCR primer nt655 #1.

XX
 Immunogenic protein; oocyst; feces; ss; antigen; antigen; cell;

XX
 T. gondii; infection; culture; Toxoplasma gondii; cell; shedding; cell;

XX
 oocyst shedding; PCR primer.

XX
 Toxoplasma gondii.

25 JUL 2000; 2000US 220593P.
 PR 16 OCT 2000; 2000US 239542P.
 PR 18 DEC 2000; 2000US 256402P.
 PR 26 FEB 2001; 2001US 271645P.
 PR 09 MAR 2001; 2001US 274809P.
 PR 13 MAR 2001; 2001US 276604P.
 XX (CURA-) (CURAGEN CORP).
 PA Padmanab M, Strydom KA, Major J, Toloczko VT, Gross WM,
 PI Szekeres FD, Alshocher JP, Burgess CE, Shinkens PA, Taupier PJ,
 PI Casman SJ, Garipalli E, MacDougall JR, Stone KL, Smithson G;
 XX WFL; 2002-106186/14.
 XX New polypeptide, useful for treating failure, anxiety, retention,
 PT depression, asthma and other conditions, the invention is directed
 PT protein receptor GPCR.
 XX Example 10; Page 129; 154pp; English.
 XX The invention relates to an isolated polypeptide protein related
 CC to the human GPCR, the amino acid sequence of which is defined by the
 CC and the polypeptide is encoded by the GPCR, the amino acid sequence
 CC polypeptide and a GPCR antibody, and useful for diagnosing
 CC treatment or preventing a GPCR-associated disorder in a human and
 CC development of a GPCR-associated disorder, and a screen detectability
 CC assay for a GPCR, a GPCR, a GPCR, a GPCR, a GPCR, a GPCR, a GPCR,
 CC related diseases including those involving the GPCR, cell growth,
 CC rate disorders, feeding disorders, and a feeding potential,
 CC directly from a GPCR, a GPCR, a GPCR, a GPCR, a GPCR, a GPCR,
 CC polypeptide, antibodies, antibodies, antibodies, antibodies, antibodies,
 CC and viral infections, pain, cancer, anxiety, pallor, asthma,
 CC Parkinson's disease, aortic heart failure, hypertension, hyperendemic,
 CC urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, anxiety disorders, myocardial
 CC infarction, ulcers, allergies, benign prostatic hyperplasia, male
 CC depression, delirium, dementia, severe mental retardation, autism,
 CC of a GPCR, a GPCR, a GPCR, a GPCR, a GPCR, a GPCR, a GPCR,
 CC Huntington's disease or Gilles de la Tourette syndrome, hematopoietic
 CC disorders, and disorders related to cell signal processing and
 CC metabolic pathway modulation. The present sequence is a forward
 CC real time quantitative PCR primer for the GPCR. Aflata used to study
 CC the tissue specific expression of GPCR.
 XX Sequence 22 BP; 8 A; 7 C; 2 G; 5 T; 0 other;
 XX Query Match: 50.74; Score 15.42; LR 24; Length 26;
 XX Best Local Similarity: 85.0%; Pred. No. 4.1e+03;
 XX Matches: 17; Conservative: 0; Mismatches: 3; Indels: 0; Gaps: 0;
 XX
 XX 10 CACCAAAACAACTACGACCA 29
 XX |||||
 XX 3 CACCAAAACAACTACGACCA 22
 XX
 XX RESULT 5
 XX AAV81225/5
 XX ID AAV81225 standard; DNA; 26 BP.
 XX AAV81225;
 XX 22 MAR 1999 (first entry)
 XX
 XX Human hpc fragment amplifying primer P001 26.
 XX
 XX Chapter 11: Proteins, Histology, Cell Biology, Anatomy, Behavior, Genetics,
 XX Growth, Development, and Physiology, Nutrition, Immunology, Infection,
 XX Invertebrate signal peptides; Human prothymosin; PCR primer; ss.
 XX Synthetic.
 XX Lama guanicoe llama.

XX W09956928-A1.
 XX 17-DEC-1998.
 XX 04-07-1999; www-nidm035.
 XX 13-JUN-1997; 97EP-0201790.
 XX (EIEF) STITCHING TEST DIFFERENTIAL PH DIFFERENTIAL.
 XX De Gans B, Harmsen MM;
 XX WFL; 1999-070327/06.
 XX New modified chaperone protein having binding site for substrate
 PT polypeptide, chaperone binding site, and secretion when
 PT is expressed with the polypeptide.
 XX Example 3; Page 19; 39pp; English.
 XX The invention relates to a modified chaperone-like protein has at least
 CC one binding site for an substrate form of a polypeptide for which,
 CC initially, it has a reduced or different binding affinity by forming
 CC a transition complex, the chaperone-like protein improves the folding of
 CC the polypeptide, and its transfer to host cells and secretion from
 CC them. Typical polypeptides that can be obtained for the complex are
 CC enzymes, proteins, proteins, proteins, proteins, proteins, proteins,
 CC for various of different types. When a polypeptide is expressed with
 CC the chaperone-like protein, yields of the polypeptide are increased by
 CC preventing formation of misfolded aggregates and by stimulating
 CC secretion of the polypeptide. With the polypeptides for growth,
 CC fitness AAV81225 is used for the PCR. Aflata used to study
 CC expression of the hpc fragment. This is used in the construction of
 CC libraries for expression of llama hpc fragment. The llama heavy chain
 CC antibodies are directed against prothymosin.
 XX Sequence 26 BP; 8 A; 7 C; 2 G; 5 T; 0 other;
 XX Query Match: 50.74; Score 15.42; LR 24; Length 26;
 XX Best Local Similarity: 85.0%; Pred. No. 4.2e+03;
 XX Matches: 17; Conservative: 0; Mismatches: 3; Indels: 0; Gaps: 0;
 XX
 XX 7 ACAACAAACAACTACGACCA 26
 XX |||||
 XX 20 ACAACAAACAACTACGACCA 1
 XX
 XX RESULT 6
 XX AAA37275
 XX ID AAA37275 standard; DNA; 24 BP.
 XX AAA37275;
 XX 09 AUG 2000 (first entry)
 XX
 XX Human PRO143 reverse PCR primer SEQ ID NO:294.
 XX
 XX Human PRO143 reverse PCR primer; 2000/07/07; 2000/07/07;
 XX Chaperone-like protein; histology, cell biology, anatomy, behavior, genetics,
 XX Growth, Development, and Physiology, Nutrition, Immunology, Infection,
 XX Invertebrate signal peptides; Human prothymosin; PCR primer; ss.
 XX Homo sapiens.
 XX W0200012708 A2.
 XX 09-MAR-2000.
 XX 01-SEP-1998; 98US-0096749.
 XX 01-SEP-1998; 98US-0096749.
 XX 01-SEP-1998; 98US-0096749.

[illegible]



```

source
1..29
/organism="synthetic construct"
/db_xref="taxon:32630"
/Note="Primer"
BASE COUNT      3 a      6 c      9 g      10 t
ORIGIN
Query Match
Best Local Similarity 70.8%; Pred. No. 1.3e+06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY      6 GAGACACCAAGACATACGCA 29
|||
28 GATACACCATATGACACATGACCA 5
Db

RESULT 39
LOCUS      A40277              30 bp      DNA      linear      PAT 05 MAR-1997
DEFINITION Sequence 9 from Patent WO9425073.
ACCESSION  A40277
VERSION     A40277.1  GI:2236373
KEYWORDS
SOURCE
Synthetic construct.
Synthetic construct.
artificial sequences.
1 (bases 1 to 30)
REFERENCE
1 Benoit,P., Deneffe,P., Pericardet,M., Seguret,S. and Vigne,E.
RECOMBINANT VIRUSES AND THEIR USE IN GENE THERAPY
Ergot: W5 942507-A 9 15 NOV-1994;
Rhone Poulenc Rorer SA (FR)
Other publication AU 6572294 941121
Other publication ZA 9403980 950119
Other publication CA 2161679 941119
Other publication FI 955154 951027
Other publication NO 954924 951026
Other publication PR 2704556 941104
Other publication BR 9406669 960130.
Location/Qualifiers
1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT      11 a      8 c      10 g      1 t
ORIGIN
Query Match
Best Local Similarity 42.7%; Score 12.8; DB 6; Length 30;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY      5 AAGACACCAAGACCA 20
|||
5 AAGACACCAAGACCA 20
Db

RESULT 40
LOCUS      ARO31959              30 bp      DNA      linear      PAT 23 SEP-1999
DEFINITION Sequence 9 from Patent US 5866551.
ACCESSION  ARO31959
VERSION     ARO31959.1  GI:5946248
KEYWORDS
SOURCE
Unknown.
Unclassified.
1 (bases 1 to 30)
REFERENCE
1 Benoit,P., Deneffe,P., Pericardet,M., Seguret,S. and Vigne,E.
RECOMBINANT VIRUSES AND THEIR USE IN GENE THERAPY
Ergot: W5 942507-A 9 15 NOV-1994;
Rhone Poulenc Rorer SA (FR)
Other publication AU 6572294 941121
Other publication ZA 9403980 950119
Other publication CA 2161679 941119
Other publication FI 955154 951027
Other publication NO 954924 951026
Other publication PR 2704556 941104
Other publication BR 9406669 960130.
Location/Qualifiers
1..30
/organism="unknown"
JOURNAL
FEATURES
source

```

```

BASE COUNT      11 a      8 c      10 g      1 t
ORIGIN
Query Match
Best Local Similarity 42.7%; Score 12.8; DB 6; Length 30;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY      5 AAGACACCAAGACCA 20
|||
5 AAGACACCAAGACCA 20
Db

```

Search completed: July 21, 2003, 14:35:00
Job time : 322.497 secs


```

REFERENCE
  1 (bases 1 to 30)
  AUTHORS
    Lashner, L. and Metzger, R.
  TITLE
    Nucleic acid sequences encoding a distal domain of the
    protein Wntless, a secretase-1 substrate.
  JOURNAL
    LASHNER, LONNIE LEE, METZGER, RAINER (ED), SCIENCE IMMUNOTHERAPY AND
    ONCOLOGY (DP)
  SOURCE
    10.1101/20041111111111
    /db_xref="taxon:32644"
  BASE COUNT
    7 a 11 c 4 g 8 t
  ORIGIN
    Query Match
    Best Local Similarity 76.2% Filed No. 1000000
    Matched 10, Conserved 10, Mismatched 1, Indels 0, Gaps 0
  CY
    10 CACCAAGAGAGCTACCTGCAAT 30
    |||||
    3 CACCATGTACAGCAGCTGCAAT 23
  RESULT 32
  107808/c
  107808
  DEFINITION
    Cytosine 4 from Patient EP 000713
  ACCESSION
    107808
  VERSION
    107808.1 01-03-00
  KEYWORDS
    .
  SOURCE
    UNKNOWN
    ORGANISM
    Unknown
    UNCLASSIFIED
  REFERENCE
    1 (bases 1 to 30)
    AUTHORS
    Faulstich, D.H., Brocke, P., Andjrosch, W. and Tress, C.
    TITLE
    Recombinant cytochrome b cytochrome b cytochrome b cytochrome b
    JOURNAL
    Biochem Biophys Res Commun 246:100-106 (1998)
  FEATUERS
    1 30
    Location/Qualifiers
    source
    1 30
    /organism="unknown"
  BASE COUNT
    3 a 7 c 4 g 14 t
  ORIGIN
    Query Match
    Best Local Similarity 76.2% Filed No. 1000000
    Matched 16, Conserved 16, Mismatched 0, Indels 0, Gaps 0
  CY
    3 ACGCGAAGAGCTACCTGCAAT 30
    |||||
    30 ACGCGAAGAGCTACCTGCAAT 30
  Db
    30 ACGCGAAGAGCTACCTGCAAT 30
  RESULT 32
  AX108722
  LOCUS
    AX108722
  DEFINITION
    Sequence 36 from Patient W00123543
  ACCESSION
    AX108722
  VERSION
    AX108722.1 GI:13923922
  KEYWORDS
    .
  SOURCE
    Synthetic construct.
    ORGANISM
    Synthetic construct.
    UNCLASSIFIED
  REFERENCE
    1 (bases 1 to 30)
    AUTHORS
    Reinhardt, C., Hahnel, A. and Tress, C.
    TITLE
    Creation of variable length and sequence linker regions for
    full-length c-myc-3' tag in c-myc-3' tag
    JOURNAL
    Patent: WO 0125443A 26-05-2001
  COMMENT
    Large Scale Biology Collection (1998)
  FEATURES
    1 31
    Location/Qualifiers
    source
    1 31
    /organism="synthetic construct"
    /db_xref="taxon:32630"
    /note="primer"
  
```

```

BASE COUNT
  5 a 6 c 12 g 8 t
  ORIGIN
    Query Match
    Best Local Similarity 76.2% Filed No. 1000000
    Matched 10, Conserved 10, Mismatched 0, Indels 0, Gaps 0
  CY
    10 CACCAAGAGAGCTACCTGCAAT 30
    |||||
    3 CACCATGTACAGCAGCTGCAAT 23
  Db
    30 ACGCGAAGAGCTACCTGCAAT 30
  RESULT 33
  BD012867/c
  107808/c
  DEFINITION
    Nucleus localizing secretase type DNA polymerase
  ACCESSION
    BD012867
  VERSION
    BD012867.1 GI:22091076
  KEYWORDS
    WO 0124495 A/90.
  SOURCE
    Synthetic construct.
    ORGANISM
    Synthetic construct.
    UNCLASSIFIED
  REFERENCE
    1 (bases 1 to 34)
    AUTHORS
    Furukawa, T., Shiga, T., Kikuchi, S. and Nishikawa, K.
    TITLE
    Nucleus localizing secretase type DNA polymerase
    JOURNAL
    Patent: WO 0124495 A 17 Apr 2001
    ACCESSION
    SECRET RESEARCH INSTITUTE CO LTD, YASUHIRO FURUKAWA, AKIHIRO NISHIKAWA,
    SAORI KIKUCHI, KAZUO NISHIKAWA
  COMMENT
    34
    Artificial sequence
    34
    WO 0124495 A/60
    PD
    12-APR-2001
    14
    25 AUG 2000 WO 2000/0905757
    PR
    05-OCT-1999 JP 99P 284001
    11
    YACHTING FORWRIGHT ARIA SHIMOMOTO SAORI KIKUCHI NISHIKAWA
    10
    CACCAAGAGAGCTACCTGCAAT 30
    |||||
    30 ACGCGAAGAGCTACCTGCAAT 30
    Location/Qualifiers
    34
    Key
    Location/Qualifiers
    34
    /organism="synthetic construct"
    /db_xref="taxon:32630"
  BASE COUNT
    6 a 10 c 6 g 12 t
  ORIGIN
    Query Match
    Best Local Similarity 65.0% Filed No. 1000000
    Matched 10, Conserved 10, Mismatched 10, Indels 0, Gaps 0
  CY
    3 CACCAAGAGAGCTACCTGCAAT 30
    |||||
    30 ACGCGAAGAGCTACCTGCAAT 30
  Db
    30 ACGCGAAGAGCTACCTGCAAT 30
  RESULT 34
  BD008322/c
  107808/c
  DEFINITION
    Standard, DNA, 34 BP.
  ACCESSION
    BD008322
  VERSION
    BD008322.1
  KEYWORDS
    .
  SOURCE
    Synthetic construct.
    ORGANISM
    Synthetic construct.
    UNCLASSIFIED
  REFERENCE
    1 (bases 1 to 34)
    AUTHORS
    Reinhardt, C., Hahnel, A. and Tress, C.
    TITLE
    Creation of variable length and sequence linker regions for
    full-length c-myc-3' tag in c-myc-3' tag
    JOURNAL
    Patent: WO 0125443A 26-05-2001
  COMMENT
    Large Scale Biology Collection (1998)
  FEATURES
    1 34
    Location/Qualifiers
    source
    1 34
    /organism="synthetic construct"
    /db_xref="taxon:32630"
    /note="primer"
  
```

Best Local Similarity 60.28, Score 13, DB 6, Length 24;
 Query Match 43.38, Score 13, DB 6, Length 24;
 Best Local Similarity 76.28, Pred. No. 1,1e+06;
 Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

LOCUS A41290
 DEFINITION Sequence 19 from Patent WO9208170.
 ACCESSION A41290
 VERSION A41290.1 GI:330394
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1 (bases 1 to 32)
 AUTHORS HUGHES, S.J., DAVIES, K.E., HIRSH, M.C. and FARMERY, A.V.
 TITLE METHOD FOR DETECTION OF THE FRASIDE X STREPTOCOCAL
 JOURNAL MEDICAL RES. COUNCIL (GB)
 MEDICAL RES. COUNCIL (GB)
 COMMENT Other Publication AU 6803094 941220.
 FEATURES
 source location/Qualifiers
 1..32
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 4 a 5 c 12 g 11 t

ORIGIN
 Query Match 44.38, Score 13, DB 6, Length 32;
 Best Local Similarity 60.28, Pred. No. 8.5e+05;
 Matches 16, Conservative 0, Mismatches 8, Indels 0, Gaps 0.

LOCUS A46203
 DEFINITION Sequence 10 from Patent WO9208170.
 ACCESSION A46203
 VERSION A46203.1 GI:330451
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1 (bases 1 to 24)
 AUTHORS MAKOFF, A.J.
 TITLE HUMAN SUBSTANTIVE REPTILES PROTEINS
 JOURNAL PATENT WO 952609-A 10 24-AUG-1995;
 WELLCOME FOUND (GB)
 FEATURES
 source location/Qualifiers
 1..24
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 5 a 4 c 12 g 11 t

ORIGIN
 Query Match 43.38, Score 13, DB 6, Length 24;
 Best Local Similarity 76.28, Pred. No. 1,1e+06;
 Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

LOCUS A46203
 DEFINITION Sequence 10 from Patent WO9208170.
 ACCESSION A46203
 VERSION A46203.1 GI:330451
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1 (bases 1 to 24)
 AUTHORS MAKOFF, A.J.
 TITLE HUMAN SUBSTANTIVE REPTILES PROTEINS
 JOURNAL PATENT WO 952609-A 10 24-AUG-1995;
 WELLCOME FOUND (GB)
 FEATURES
 source location/Qualifiers
 1..24
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 5 a 4 c 12 g 11 t

ORIGIN

LOCUS A41290
 DEFINITION Sequence 19 from Patent WO9208170.
 ACCESSION A41290
 VERSION A41290.1 GI:330394
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1 (bases 1 to 32)
 AUTHORS HUGHES, S.J., DAVIES, K.E., HIRSH, M.C. and FARMERY, A.V.
 TITLE METHOD FOR DETECTION OF THE FRASIDE X STREPTOCOCAL
 JOURNAL MEDICAL RES. COUNCIL (GB)
 MEDICAL RES. COUNCIL (GB)
 COMMENT Other Publication AU 6803094 941220.
 FEATURES
 source location/Qualifiers
 1..32
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 4 a 5 c 12 g 11 t

ORIGIN
 Query Match 43.38, Score 13, DB 6, Length 24;
 Best Local Similarity 76.28, Pred. No. 1,1e+06;
 Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

LOCUS A46203
 DEFINITION Sequence 10 from Patent WO9208170.
 ACCESSION A46203
 VERSION A46203.1 GI:330451
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1 (bases 1 to 24)
 AUTHORS MAKOFF, A.J.
 TITLE HUMAN SUBSTANTIVE REPTILES PROTEINS
 JOURNAL PATENT WO 952609-A 10 24-AUG-1995;
 WELLCOME FOUND (GB)
 FEATURES
 source location/Qualifiers
 1..24
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 5 a 4 c 12 g 11 t

ORIGIN
 Query Match 43.38, Score 13, DB 6, Length 24;
 Best Local Similarity 76.28, Pred. No. 1,1e+06;
 Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

LOCUS A46203
 DEFINITION Sequence 10 from Patent WO9208170.
 ACCESSION A46203
 VERSION A46203.1 GI:330451
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1 (bases 1 to 24)
 AUTHORS MAKOFF, A.J.
 TITLE HUMAN SUBSTANTIVE REPTILES PROTEINS
 JOURNAL PATENT WO 952609-A 10 24-AUG-1995;
 WELLCOME FOUND (GB)
 FEATURES
 source location/Qualifiers
 1..24
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 5 a 4 c 12 g 11 t

ORIGIN

SOURCE
HUMAN
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Cephalochordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

REFERENCE
1
TITLE
Obesity associated kallikrein-like peptidases
JOURNAL
GENSKI (FR)

FEATURES
Source
Location/Qualifiers
1..18 /db_xref="taxon:9606"
/db_xref="taxon:9606"
1..18 /note="Peptidase amplification primer: 22-2222 for SEQ 22"

BASE COUNT
0 a 4 c 4 g 10 t

ORIGIN

Query Match 44.0%, Score 13.2, DB 6, Length 18,
Best Local Similarity 43.3%, Prod No 9.9e+05,
Matches 15; Conservative 0; Mismatches 3; Indels 3; Gaps 3.

AX104191.1 GI:13920378

DEFINITION
Sequence 15 from Patent WO 02/000000

ACCESSION
AX104191

VERSION
AX104191.1 GI:13920378

KEYWORDS
Synthetic construct
artificial sequences
1..18 bases (1 to 26)

REFERENCE
Krieg, A.M., Schreier, C. and Vasilov, D.C.
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: WO 0122972-A 373 05-APR-2001

SOURCE
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) / JOEY PHARMACEUTICALS GmbH (DE)

REFERENCE
1
TITLE
Obesity associated kallikrein-like peptidases
JOURNAL
GENSKI (FR)

FEATURES
Source
Location/Qualifiers
1..18 /db_xref="taxon:9606"
/db_xref="taxon:9606"
1..18 /note="Peptidase amplification primer: 22-2222 for SEQ 22"

BASE COUNT
0 a 4 c 4 g 10 t

ORIGIN

Query Match 44.0%, Score 13.2, DB 6, Length 18,
Best Local Similarity 43.3%, Prod No 9.9e+05,
Matches 15; Conservative 0; Mismatches 3; Indels 3; Gaps 3.

AX104191.1 GI:13920378

DEFINITION
Sequence 15 from Patent US 5707796

ACCESSION
AX104191

VERSION
AX104191.1 GI:13920378

KEYWORDS
Synthetic construct
artificial sequences
1..18 bases (1 to 26)

REFERENCE
Krieg, A.M., Schreier, C. and Vasilov, D.C.
TITLE
Immunostimulatory nucleic acids
JOURNAL
Patent: US 5707796 A 11 13 JAN 1999

Query Match 47.2% Score 14.2 DB 12 Length 20
 Best Local Similarity 94.2% Pred. No. 3.5e+05
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGACGACCAAGACACTAC 21
 |||||
 26 CAGACGACCAAGACACTAC 2

RESULT 8
 AX037433
 DEFINITION Sequence 72 from Patent WO0175165.
 ACCESSION AX037433
 VERSION AX037433.1 GI:16542010
 KEYWORDS
 SOURCE Synthetic construct.
 ORGANISM Artificial sequences.

REFERENCE 1
 AUTHORs M. A. Thiede, M. A. Thiede, F. B. Thiede, J. T. A. Haid, T. Messersmith, E. and Haid, F.
 TITLE Screening methods and methods for identifying putative disorders
 JOURNAL J. Clin. Invest. 113:1157-1165, 2001.

FEATURES
 LOCATION/Qualifiers
 1..29
 /organism="synthetic construct"
 /db_xref="taxon:83290"
 /note="probe 1717"

BASE COUNT 12 a 8 c 6 g 3 t
 ORIGIN

Query Match 46.7% Score 14.2 DB 12 Length 20
 Best Local Similarity 90.2% Pred. No. 3.5e+05
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GACGACCAAGACACTAC 29
 |||||
 8 GACGACCAAGACACTAC 29

RESULT 9
 AR137319/c
 LOCUS AR137319 20 bp DNA Linear PAT 16 JUN 2001
 DEFINITION Sequence 66 from Patent US 6197505.
 ACCESSION AR137319
 VERSION AR137319.1 GI:1478820
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1
 AUTHORs Thiede, M.A. and Malavale, G.
 TITLE Regulation of hematopoietic stem cell differentiation by the use of
 JOURNAL J. Clin. Invest. 113:1157-1165, 2001.

FEATURES
 LOCATION/Qualifiers
 1..20
 /organism="unknown"

BASE COUNT 1 a 6 c 5 g 8 t
 ORIGIN

Query Match 46.7% Score 14.2 DB 12 Length 20
 Best Local Similarity 88.2% Pred. No. 3.5e+05
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGACGACCAAGACACTAC 20
 |||||
 19 AAGACGACCAAGACACTAC 3

RESULT 10
 AR137319/c
 LOCUS AR137319 20 bp DNA Linear PAT 16 JUN 2001
 DEFINITION Sequence 66 from Patent US 6197505.
 ACCESSION AR137319
 VERSION AR137319.1 GI:1478820
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
 AUTHORs Thiede, M.A. and Malavale, G.
 TITLE Regulation of hematopoietic stem cell differentiation by the use of
 JOURNAL J. Clin. Invest. 113:1157-1165, 2001.

FEATURES
 LOCATION/Qualifiers
 1..20
 /organism="unknown"

BASE COUNT 1 a 6 c 5 g 8 t
 ORIGIN

Query Match 46.7% Score 14.2 DB 12 Length 20
 Best Local Similarity 88.2% Pred. No. 3.5e+05
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AAGACGACCAAGACACTAC 20
 |||||
 19 AAGACGACCAAGACACTAC 3

RESULT 11
 AX037433
 LOCUS AX037433 20 bp DNA Linear PAT 16 JUN 2001
 DEFINITION Sequence 72 from Patent WO0175165.
 ACCESSION AX037433
 VERSION AX037433.1 GI:16542010
 KEYWORDS
 SOURCE Synthetic construct.
 ORGANISM Artificial sequences.

REFERENCE 1 (bases 1 to 20)
 AUTHORs Thiede, M.A. and Malavale, G.
 TITLE Regulation of hematopoietic stem cell differentiation by the use of
 JOURNAL J. Clin. Invest. 113:1157-1165, 2001.

FEATURES
 LOCATION/Qualifiers
 1..20
 /organism="unknown"

BASE COUNT 9 a 5 c 5 g 1 t
 ORIGIN

Query Match 46.7% Score 14.2 DB 12 Length 20
 Best Local Similarity 88.2% Pred. No. 3.5e+05
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GACGACCAAGACACTAC 24
 |||||
 3 GACGACCAAGACACTAC 19

RESULT 12
 AX037433/c
 LOCUS AX037433 20 bp DNA Linear PAT 16 JUN 2001
 DEFINITION Sequence 72 from Patent WO0175165.
 ACCESSION AX037433
 VERSION AX037433.1 GI:16542010
 KEYWORDS
 SOURCE Synthetic construct.
 ORGANISM Artificial sequences.

REFERENCE 1 (bases 1 to 20)
 AUTHORs Thiede, M.A. and Malavale, G.
 TITLE Regulation of hematopoietic stem cell differentiation by the use of
 JOURNAL J. Clin. Invest. 113:1157-1165, 2001.

FEATURES
 LOCATION/Qualifiers
 1..20
 /organism="unknown"

BASE COUNT 9 a 5 c 5 g 1 t
 ORIGIN

Query Match 46.7% Score 14.2 DB 12 Length 20
 Best Local Similarity 88.2% Pred. No. 3.5e+05
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GACGACCAAGACACTAC 24
 |||||
 3 GACGACCAAGACACTAC 19

[illegible][illegible]

C 356	11.4	14.0	14	4	AP089746	AP089746 Sequence	C 431	11.2	17.4	28	6	Pos114	Pos114 Ref. contig
C 359	11.4	14.0	14	6	AP089717	AP089717 Sequence	C 432	11.2	17.3	29	6	AP107038	AP107038 Sequence
C 360	11.4	14.0	15	6	AP112445	AP112445 Sequence	C 433	11.2	17.3	29	10	MS130256	MS130256 Sequence
C 361	11.4	14.0	15	6	AX055447	AX055447 Sequence	C 434	11.2	17.3	29	6	AP004741	AP004741 Sequence
C 362	11.4	14.0	16	6	FL0647	FL0647 Probe for d	C 435	11.2	17.3	30	6	AP106449	AP106449 Sequence
C 363	11.4	14.0	16	6	FL0643	FL0643 Probe for d	C 436	11.2	17.3	30	6	AP117012	AP117012 Sequence
C 364	11.4	14.0	16	6	EL1443	EL1443 Linker 3/1	C 437	11.2	17.3	30	6	AP036572	AP036572 Sequence
C 365	11.2	17.3	17	6	AX421676	AX421676 Sequence	C 438	11.2	17.3	30	6	AP001144	AP001144 Sequence
C 366	11.2	17.3	17	6	AR093667	AR093667 Sequence	C 439	11.2	17.3	30	6	AP117857	AP117857 Sequence
C 367	11.2	17.3	18	6	AP106482	AP106482 Sequence	C 440	11.2	17.3	30	6	FL04246	FL04246 Sequence
C 368	11.2	17.3	18	6	AX017251	AX017251 Sequence	C 441	11.2	17.3	30	6	FL02801	FL02801 Sequence
C 369	11.2	17.3	18	12	AP069479	AP069479 Sequence	C 442	11.2	17.3	30	6	FL07012	FL07012 Sequence
C 370	11.2	17.3	19	6	AP069479	AP069479 Sequence	C 443	11.2	17.3	30	6	FL01004	FL01004 Sequence
C 371	11.2	17.3	19	6	AX119248	AX119248 Sequence	C 444	11.2	17.3	30	6	FL01104	FL01104 Sequence
C 372	11.2	17.3	19	6	AX379456	AX379456 Sequence	C 445	11.2	17.3	31	6	AP031712	AP031712 Sequence
C 373	11.2	17.3	19	6	AX378651	AX378651 Sequence	C 446	11.2	17.3	31	6	AP062466	AP062466 Sequence
C 374	11.2	17.3	19	6	AX419131	AX419131 Sequence	C 447	11.2	17.3	31	6	AR067942	AR067942 Sequence
C 375	11.2	17.3	19	6	AX474779	AX474779 Sequence	C 448	11.2	17.3	31	6	AR050241	AR050241 Sequence
C 376	11.2	17.3	19	6	FL06941	FL06941 Sequence	C 449	11.2	17.3	31	6	AP166981	AP166981 Sequence
C 377	11.2	17.3	20	6	AX458713	AX458713 Sequence	C 450	11.2	17.3	31	6	AP107732	AP107732 Sequence
C 378	11.2	17.3	20	6	AP106818	AP106818 Sequence	C 451	11.2	17.3	31	6	AP036901	AP036901 Sequence
C 379	11.2	17.3	20	6	AX419741	AX419741 Sequence	C 452	11.2	17.3	31	6	AX007090	AX007090 Sequence
C 380	11.2	17.3	20	6	AX419742	AX419742 Sequence	C 453	11.2	17.3	31	6	AX424285	AX424285 Sequence
C 381	11.2	17.3	20	6	AX419743	AX419743 Sequence	C 454	11.2	17.3	31	6	AX046646	AX046646 Sequence
C 382	11.2	17.3	20	6	AX468713	AX468713 Sequence	C 455	11.2	17.3	31	6	AX429440	AX429440 Sequence
C 383	11.2	17.3	20	6	AX458712	AX458712 Sequence	C 456	11.2	17.3	31	6	FL002942	FL002942 Sequence
C 384	11.2	17.3	20	6	FL1157	FL1157 Sequence	C 457	11.2	17.3	31	6	FL02264	FL02264 Sequence
C 385	11.2	17.3	21	6	AX035214	AX035214 Sequence	C 458	11.2	17.3	31	6	AR135346	AR135346 Sequence
C 386	11.2	17.3	21	6	AX005250	AX005250 Sequence	C 459	11.2	17.3	32	6	AR145447	AR145447 Sequence
C 387	11.2	17.3	22	6	AX039526	AX039526 Sequence	C 460	11.2	17.3	32	6	AX136837	AX136837 Sequence
C 388	11.2	17.3	22	6	AX441755	AX441755 Sequence	C 461	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 389	11.2	17.3	22	6	AX441756	AX441756 Sequence	C 462	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 390	11.2	17.3	22	6	AX441757	AX441757 Sequence	C 463	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 391	11.2	17.3	22	6	AX441758	AX441758 Sequence	C 464	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 392	11.2	17.3	22	6	AX441759	AX441759 Sequence	C 465	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 393	11.2	17.3	22	6	AP069081	AP069081 Sequence	C 466	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 394	11.2	17.3	24	6	AR154074	AR154074 Sequence	C 467	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 395	11.2	17.3	24	6	AR173114	AR173114 Sequence	C 468	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 396	11.2	17.3	24	6	AX039527	AX039527 Sequence	C 469	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 397	11.2	17.3	24	6	AX039528	AX039528 Sequence	C 470	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 398	11.2	17.3	24	6	AX151865	AX151865 Sequence	C 471	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 399	11.2	17.3	24	6	AX151866	AX151866 Sequence	C 472	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 400	11.2	17.3	24	6	AX151867	AX151867 Sequence	C 473	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 401	11.2	17.3	24	6	AX151868	AX151868 Sequence	C 474	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 402	11.2	17.3	24	6	AX151869	AX151869 Sequence	C 475	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 403	11.2	17.3	24	6	AX151870	AX151870 Sequence	C 476	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 404	11.2	17.3	24	6	AX151871	AX151871 Sequence	C 477	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 405	11.2	17.3	24	6	AX151872	AX151872 Sequence	C 478	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 406	11.2	17.3	24	6	AX151873	AX151873 Sequence	C 479	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 407	11.2	17.3	24	6	AX151874	AX151874 Sequence	C 480	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 408	11.2	17.3	24	6	AX151875	AX151875 Sequence	C 481	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 409	11.2	17.3	24	6	AX151876	AX151876 Sequence	C 482	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 410	11.2	17.3	24	6	AX151877	AX151877 Sequence	C 483	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 411	11.2	17.3	24	6	AX151878	AX151878 Sequence	C 484	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 412	11.2	17.3	24	6	AX151879	AX151879 Sequence	C 485	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 413	11.2	17.3	24	6	AX151880	AX151880 Sequence	C 486	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 414	11.2	17.3	24	6	AX151881	AX151881 Sequence	C 487	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 415	11.2	17.3	24	6	AX151882	AX151882 Sequence	C 488	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 416	11.2	17.3	24	6	AX151883	AX151883 Sequence	C 489	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 417	11.2	17.3	24	6	AX151884	AX151884 Sequence	C 490	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 418	11.2	17.3	24	6	AX151885	AX151885 Sequence	C 491	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 419	11.2	17.3	24	6	AX151886	AX151886 Sequence	C 492	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 420	11.2	17.3	24	6	AX151887	AX151887 Sequence	C 493	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 421	11.2	17.3	24	6	AX151888	AX151888 Sequence	C 494	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 422	11.2	17.3	24	6	AX151889	AX151889 Sequence	C 495	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 423	11.2	17.3	24	6	AX151890	AX151890 Sequence	C 496	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 424	11.2	17.3	24	6	AX151891	AX151891 Sequence	C 497	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 425	11.2	17.3	24	6	AX151892	AX151892 Sequence	C 498	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 426	11.2	17.3	24	6	AX151893	AX151893 Sequence	C 499	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 427	11.2	17.3	24	6	AX151894	AX151894 Sequence	C 500	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 428	11.2	17.3	24	6	AX151895	AX151895 Sequence	C 501	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 429	11.2	17.3	24	6	AX151896	AX151896 Sequence	C 502	11.2	17.3	32	6	FL14548	FL14548 Sequence
C 430	11.2	17.3	24	6	AX151897	AX151897 Sequence	C 503	11.2	17.3	32	6	FL14548	FL14548 Sequence

•
•

FEATURES
Source

1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Satoch" unpublished cDNA library, young
adult"
/issue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBluescript SK"
BASE COUNT
ORIGIN

Query Match 42.7%, Score 12.8, DB 10, Length 34,
Best Local Similarity 70.8%, Pred. No. 3e+05;
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;
2Y 6 TGGCCAGGAGGAGATGTTTCTG 29
|||||
1 TTGGAGAGAGGAGGTTTCTTCT 24

RESULT 37
LOCUS AV953949 34 bp mRNA linear EST 14 MAR 2002
DEFINITION AV953949 Rat Satch of Akita University young adult cDNA
intestinalis cDNA clone clon9918 5', mRNA sequence.
ACCESSION AV953949 GI:19442248
VERSION EST
KEYWORDS Clona intestinalis.
SOURCE Clona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Artiodactyla; Perissodactyla;
Phlebotominae; Clonidae; Clona.

REFERENCE 1 (bases 1 to 34)
Satoch, N., Satoch, Y., Kobata, Y. and Shin, I.T.
Expressed genes in Clona intestinalis
Unpublished (2000)
TITLE
JOURNAL
COMMENT
Contact: Mori Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-706-1113
Email: satch@zoology.kyoto-u.ac.jp

FEATURES
Source
1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Satoch" unpublished cDNA library, young
adult"
/issue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBluescript SK"
BASE COUNT
ORIGIN

Query Match 42.7%, Score 12.8, DB 10, Length 34,
Best Local Similarity 70.8%, Pred. No. 3e+05;
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;
2Y 6 TGGCCAGGAGGAGATGTTTCTG 29
|||||
1 TTGGAGAGAGGAGGTTTCTTCT 24

RESULT 38
LOCUS AV957202 34 bp mRNA linear EST 14 MAR 2002
DEFINITION AV957202 Rat Satch of Akita University young adult cDNA
intestinalis cDNA clone clon9919 5', mRNA sequence.

ACCESSION AV957202
VERSION AV957202 GI:19444601
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Artiodactyla; Perissodactyla;
Phlebotominae; Clonidae; Clona.

REFERENCE 1 (bases 1 to 34)
Satoch, N., Satoch, Y., Kobata, Y. and Shin, I.T.
Expressed genes in Clona intestinalis
Unpublished (2000)
TITLE
JOURNAL
COMMENT
Contact: Mori Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-706-1113
Email: satch@zoology.kyoto-u.ac.jp

FEATURES
Source
1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Satoch" unpublished cDNA library, young
adult"
/issue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBluescript SK"
BASE COUNT
ORIGIN

Query Match 42.7%, Score 12.8, DB 10, Length 34,
Best Local Similarity 70.8%, Pred. No. 3e+05;
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;
2Y 6 TGGCCAGGAGGAGATGTTTCTG 29
|||||
1 TTGGAGAGAGGAGGTTTCTTCT 24

RESULT 39
LOCUS AV958100 34 bp mRNA linear EST 14 MAR 2002
DEFINITION AV958100 Rat Satch of Akita University young adult cDNA
intestinalis cDNA clone clon9918 5', mRNA sequence.
ACCESSION AV958100 GI:19446199
VERSION EST.
KEYWORDS Clona intestinalis.
SOURCE Clona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Artiodactyla; Perissodactyla;
Phlebotominae; Clonidae; Clona.

REFERENCE 1 (bases 1 to 34)
Satoch, N., Satoch, Y., Kobata, Y. and Shin, I.T.
Expressed genes in Clona intestinalis
Unpublished (2000)
TITLE
JOURNAL
COMMENT
Contact: Mori Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-706-1113
Email: satch@zoology.kyoto-u.ac.jp

FEATURES
Source
1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Satoch" unpublished cDNA library, young
adult"
/issue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBluescript SK"
BASE COUNT
ORIGIN

REFERENCE
1 (bases 1 to 34)
AUTHORS
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Saitoh
Department of Zoology
Kyoto University
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Email: saito@zoology.kyoto-u.ac.jp

FEATURES
source
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="North Saitoh unpublished cDNA library, young adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBluescript SK"

BASE COUNT
a 4
c 3
g 3
t 17

ORIGIN
Query Match 42.7%, E-value 12.5, 12.1%, Length 34,
Best local similarity 70.6%, Field No. J05057
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0,
1 TCGGACGAGCGGATTTTCTT 24

RESULT 31
AV953797
LOCUS
AV953797 North Saitoh unpublished cDNA library, young adult *Ciona*
intestinalis cDNA clone c1059324, cDNA sequence.
VERSION
AV953797
KEYWORDS
EST.
EST: 19442096
SOURCE
Ciona intestinalis
Ciona intestinalis
Eukaryota, Metazoa, Chordata, Vertebrata, Ascidiacea, Aplousobranchia,
Phlebobranchia, Clonidae, *Ciona*.
REFERENCE
1 (bases 1 to 34)
AUTHORS
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Saitoh
Department of Zoology
Kyoto University
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Email: saito@zoology.kyoto-u.ac.jp

FEATURES
source
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="North Saitoh unpublished cDNA library, young adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBluescript SK"

BASE COUNT
a 2
c 3
g 3
t 17

ORIGIN
Query Match 42.7%, E-value 12.5, 12.1%, Length 34,
Best local similarity 70.6%, Field No. J05057
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0,
1 TCGGACGAGCGGATTTTCTT 24

RESULT 35
AV953843
LOCUS
AV953843 North Saitoh unpublished cDNA library, young adult *Ciona*
intestinalis cDNA clone c1059324, cDNA sequence.
VERSION
AV953843
KEYWORDS
EST.
EST: 31194112
SOURCE
Ciona intestinalis
Ciona intestinalis
Eukaryota, Metazoa, Chordata, Vertebrata, Ascidiacea, Aplousobranchia,
Phlebobranchia, Clonidae, *Ciona*.
REFERENCE
1 (bases 1 to 34)
AUTHORS
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Saitoh
Department of Zoology
Kyoto University
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Email: saito@zoology.kyoto-u.ac.jp

FEATURES
source
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="North Saitoh unpublished cDNA library, young adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBluescript SK"

BASE COUNT
a 2
c 3
g 3
t 17

ORIGIN
Query Match 42.7%, E-value 12.5, 12.1%, Length 34,
Best local similarity 70.6%, Field No. J05057
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0,
1 TCGGACGAGCGGATTTTCTT 24

RESULT 36
AV953896
LOCUS
AV953896 North Saitoh unpublished cDNA library, young adult *Ciona*
intestinalis cDNA clone c1059324, cDNA sequence.
VERSION
AV953896
KEYWORDS
EST.
EST: 31194115
SOURCE
Ciona intestinalis
Ciona intestinalis
Eukaryota, Metazoa, Chordata, Vertebrata, Ascidiacea, Aplousobranchia,
Phlebobranchia, Clonidae, *Ciona*.
REFERENCE
1 (bases 1 to 34)
AUTHORS
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Saitoh
Department of Zoology
Kyoto University
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Email: saito@zoology.kyoto-u.ac.jp

FEATURES
source
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="North Saitoh unpublished cDNA library, young adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBluescript SK"

BASE COUNT
a 2
c 3
g 3
t 17

ORIGIN
Query Match 42.7%, E-value 12.5, 12.1%, Length 34,
Best local similarity 70.6%, Field No. J05057
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0,
1 TCGGACGAGCGGATTTTCTT 24

RESULT 32
 AV947929 34 bp mRNA linear EST 14 MAR 2002
 LOCUS
 DEFINITION AV947929 Not Satoh unpublished cDNA library, young adult, Clona
 intestinalis cDNA clone clado00057, mRNA sequence.
 AV947929
 ACCESSION
 VERSION AV947929.1 GI:19428688
 KEYWORDS
 SOURCE EST
 ORGANISM Clona intestinalis
 Clona intestinalis
 Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euryptera,
 Phlebobranchia/Clonidae/Clona.
 1 (bases 1 to 34)
 Satch.N., Satoh.Y., Kohara.Y. and Shimizu.T.
 Unpublished genes in Clona intestinalis
 Unpublished (2000)
 CONTACT: Nori Satoh
 Department of Zoology
 Kyoto University
 Kyoto 606-8501, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-753-4081
 Email: satchi@zoology.kyoto-u.ac.jp
 FEATURES
 SOURCE
 1 34
 /organism="Clona intestinalis"
 /db_xref="taxon:7719"
 /clone_lib="not satoh unpublished cDNA library, young
 adult"
 /cdate="1999-11-01"
 /csize="34bp"
 /cstype="young adult"
 /dovstage="young adult"
 /note="Vector: pBluescript SK"
 ORIGIN
 1 TTGGACGAGAGTTTCTTTT 24

RESULT 31
 AV947922 34 bp mRNA linear EST 14 MAR 2002
 LOCUS
 DEFINITION AV947922 Not Satoh unpublished cDNA library, young adult, Clona
 intestinalis cDNA clone clado00057, mRNA sequence.
 AV947922
 ACCESSION
 VERSION AV947922.1 GI:19437921
 KEYWORDS
 SOURCE EST
 ORGANISM Clona intestinalis
 Clona intestinalis
 Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euryptera,
 Phlebobranchia/Clonidae/Clona.
 1 (bases 1 to 34)
 Satch.N., Satoh.Y., Kohara.Y. and Shimizu.T.
 Unpublished genes in Clona intestinalis
 Unpublished (2000)
 CONTACT: Nori Satoh
 Department of Zoology
 Kyoto University
 Kyoto 606-8501, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-753-4081
 Email: satchi@zoology.kyoto-u.ac.jp
 FEATURES
 SOURCE
 1 34
 /organism="Clona intestinalis"
 /db_xref="taxon:7719"
 /clone_lib="not satoh unpublished cDNA library, young
 adult"
 /cdate="1999-11-01"
 /csize="34bp"
 /cstype="young adult"
 /dovstage="young adult"
 /note="Vector: pBluescript SK"
 ORIGIN
 1 TTGGACGAGAGTTTCTTTT 24

RESULT 30
 AV947921 34 bp mRNA linear EST 14 MAR 2002
 LOCUS
 DEFINITION AV947921 Not Satoh unpublished cDNA library, young adult, Clona
 intestinalis cDNA clone clado00057, mRNA sequence.
 AV947921
 ACCESSION
 VERSION AV947921.1 GI:19436620
 KEYWORDS
 SOURCE EST
 ORGANISM Clona intestinalis
 Clona intestinalis
 Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euryptera,
 Phlebobranchia/Clonidae/Clona.
 1 (bases 1 to 34)
 Satch.N., Satoh.Y., Kohara.Y. and Shimizu.T.
 Unpublished genes in Clona intestinalis
 Unpublished (2000)
 CONTACT: Nori Satoh
 Department of Zoology
 Kyoto University
 Kyoto 606-8501, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-753-4081
 Email: satchi@zoology.kyoto-u.ac.jp
 FEATURES
 SOURCE
 1 34
 /organism="Clona intestinalis"
 /db_xref="taxon:7719"
 /clone_lib="not satoh unpublished cDNA library, young
 adult"
 /cdate="1999-11-01"
 /csize="34bp"
 /cstype="young adult"
 /dovstage="young adult"
 /note="Vector: pBluescript SK"
 ORIGIN
 1 TTGGACGAGAGTTTCTTTT 24

RESULT 32
 AV947921 34 bp mRNA linear EST 14 MAR 2002
 LOCUS
 DEFINITION AV947921 Not Satoh unpublished cDNA library, young adult, Clona
 intestinalis cDNA clone clado00057, mRNA sequence.
 AV947921
 ACCESSION
 VERSION AV947921.1 GI:19436620
 KEYWORDS
 SOURCE EST
 ORGANISM Clona intestinalis
 Clona intestinalis
 Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euryptera,
 Phlebobranchia/Clonidae/Clona.
 1 (bases 1 to 34)
 Satch.N., Satoh.Y., Kohara.Y. and Shimizu.T.
 Unpublished genes in Clona intestinalis
 Unpublished (2000)
 CONTACT: Nori Satoh
 Department of Zoology
 Kyoto University
 Kyoto 606-8501, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-753-4081
 Email: satchi@zoology.kyoto-u.ac.jp
 FEATURES
 SOURCE
 1 34
 /organism="Clona intestinalis"
 /db_xref="taxon:7719"
 /clone_lib="not satoh unpublished cDNA library, young
 adult"
 /cdate="1999-11-01"
 /csize="34bp"
 /cstype="young adult"
 /dovstage="young adult"
 /note="Vector: pBluescript SK"
 ORIGIN
 1 TTGGACGAGAGTTTCTTTT 24

RESULT 31
 AV947922 34 bp mRNA linear EST 14 MAR 2002
 LOCUS
 DEFINITION AV947922 Not Satoh unpublished cDNA library, young adult, Clona
 intestinalis cDNA clone clado00057, mRNA sequence.
 AV947922
 ACCESSION
 VERSION AV947922.1 GI:19437921
 KEYWORDS
 SOURCE EST
 ORGANISM Clona intestinalis
 Clona intestinalis
 Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euryptera,
 Phlebobranchia/Clonidae/Clona.
 1 (bases 1 to 34)
 Satch.N., Satoh.Y., Kohara.Y. and Shimizu.T.
 Unpublished genes in Clona intestinalis
 Unpublished (2000)
 CONTACT: Nori Satoh
 Department of Zoology
 Kyoto University
 Kyoto 606-8501, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-753-4081
 Email: satchi@zoology.kyoto-u.ac.jp
 FEATURES
 SOURCE
 1 34
 /organism="Clona intestinalis"
 /db_xref="taxon:7719"
 /clone_lib="not satoh unpublished cDNA library, young
 adult"
 /cdate="1999-11-01"
 /csize="34bp"
 /cstype="young adult"
 /dovstage="young adult"
 /note="Vector: pBluescript SK"
 ORIGIN
 1 TTGGACGAGAGTTTCTTTT 24

RESULT 30
 AV947921 34 bp mRNA linear EST 14 MAR 2002
 LOCUS
 DEFINITION AV947921 Not Satoh unpublished cDNA library, young adult, Clona
 intestinalis cDNA clone clado00057, mRNA sequence.
 AV947921
 ACCESSION
 VERSION AV947921.1 GI:19436620
 KEYWORDS
 SOURCE EST
 ORGANISM Clona intestinalis
 Clona intestinalis
 Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euryptera,
 Phlebobranchia/Clonidae/Clona.
 1 (bases 1 to 34)
 Satch.N., Satoh.Y., Kohara.Y. and Shimizu.T.
 Unpublished genes in Clona intestinalis
 Unpublished (2000)
 CONTACT: Nori Satoh
 Department of Zoology
 Kyoto University
 Kyoto 606-8501, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-753-4081
 Email: satchi@zoology.kyoto-u.ac.jp
 FEATURES
 SOURCE
 1 34
 /organism="Clona intestinalis"
 /db_xref="taxon:7719"
 /clone_lib="not satoh unpublished cDNA library, young
 adult"
 /cdate="1999-11-01"
 /csize="34bp"
 /cstype="young adult"
 /dovstage="young adult"
 /note="Vector: pBluescript SK"
 ORIGIN
 1 TTGGACGAGAGTTTCTTTT 24

Matches 17, Conserved 0, Mismatches 7, Indels 0, Gaps 0

QY 6 TCGGACGAGGAGTTCCT 29
 1 TCGGACGAGGAGTTCCT 24

db 1 TCGGACGAGGAGTTCCT 24

RESULT 27
 AV959917 33 bp mRNA linear EST 14 MAR 2002
 LOCUS AV959917
 DEFINITION AV959917 Nov 2001. Sato unpublished cDNA library, young adult Clona
 intestinalis cDNA clone cl1011045, mRNA sequence.
 ACCESSION AV959917
 VERSION AV959917.1 GI:1947016
 KEYWORDS EST.
 SOURCE Clona intestinalis
 ORGANISM Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euteleostomi,
 Phlebobranchia, Clonidae, Clona.

REFERENCE 1 (bases 1 to 33)
 Sato, N., Satchu, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Clona intestinalis
 Unpublished (2000)

AUTHORS Satchu, N., Satchu, Y., Kohara, Y. and Shin-i, T.
 TITLE Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2000)
 COMMENT Contact: Naito Satchu
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satchu@zoology.kyoto-u.ac.jp
 Location/Jaliffiers

FEATURES
 source
 1..34
 /organism="Clona intestinalis"
 /db_xref="taxon:7919"
 /note="Vector: pBluescript SK"

BASE COUNT
 2 a 5 c 6 g 19 t

ORIGIN
 Query Match 42.7% Score 12.8, DB 109 Length 33
 Best local similarity: 70.0% (Seq. No. 26405)
 Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0

QY 6 TCGGACGAGGAGTTCCT 29
 1 TCGGACGAGGAGTTCCT 24

db 1 TCGGACGAGGAGTTCCT 24

RESULT 28
 AV931499 34 bp mRNA linear EST 21 JUN 2001
 LOCUS AV931499
 DEFINITION AV931499 K. Sato unpublished cDNA library, Hordium vulgare subsp.
 vulgare, species determination Hordium vulgare subsp. vulgare cDNA
 clone bags3918, mRNA sequence.
 ACCESSION AV931499
 VERSION AV931499.1 GI:1462579
 KEYWORDS EST.
 SOURCE Hordium vulgare subsp. vulgare
 ORGANISM Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euteleostomi,
 Cyprinodontiformes, Cyprinodontidae, Hordium.
 TITLE Hordium vulgare subsp. vulgare
 JOURNAL Unpublished (2001)
 COMMENT Contact: Katsuhiko Sato
 Research Institute for Bioresearches
 Okayama University, Bailey Germplasm Center

Contact: Naito Satchu, Kyoto University, Japan
 Email: kazu@zoology.kyoto-u.ac.jp
 URL: <http://www.zoology.kyoto-u.ac.jp/~satchu/>
 Sato, N., Satchu, Y., Kohara, Y., Shin-i, T. and Kohara, Y. Direct
 submission:
 database: <http://www.ncbi.nlm.nih.gov/BLAST/Barley.html>
 Location/Jaliffiers

FEATURES
 source
 1..34
 /organism="Hordium vulgare subsp. vulgare"
 /db_xref="taxon:12509"
 /note="Vector: pBluescript SK"

BASE COUNT
 2 a 5 c 6 g 19 t

ORIGIN
 Query Match 42.7% Score 12.8, DB 109 Length 34
 Best local similarity: 70.0% (Seq. No. 26405)
 Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0

QY 6 TCGGACGAGGAGTTCCT 29
 1 TCGGACGAGGAGTTCCT 24

db 1 TCGGACGAGGAGTTCCT 24

RESULT 29
 AV947813 34 bp mRNA linear EST 17 MAR 2002
 LOCUS AV947813
 DEFINITION AV947813 North Satchu unpublished cDNA library, young adult Clona
 intestinalis cDNA clone cl1011045, mRNA sequence.
 ACCESSION AV947813
 VERSION AV947813.1 GI:1947022
 KEYWORDS EST.
 SOURCE Clona intestinalis
 ORGANISM Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euteleostomi,
 Phlebobranchia, Clonidae, Clona.

REFERENCE 1 (bases 1 to 34)
 Satchu, N., Satchu, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Clona intestinalis
 Unpublished (2000)

AUTHORS Satchu, N., Satchu, Y., Kohara, Y. and Shin-i, T.
 TITLE Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2000)
 COMMENT Contact: Naito Satchu
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satchu@zoology.kyoto-u.ac.jp
 Location/Jaliffiers

FEATURES
 source
 1..34
 /organism="Clona intestinalis"
 /db_xref="taxon:7919"
 /note="Vector: pBluescript SK"

BASE COUNT
 2 a 5 c 6 g 19 t

ORIGIN
 Query Match 42.7% Score 12.8, DB 109 Length 34
 Best local similarity: 70.0% (Seq. No. 26405)
 Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0

QY 6 TCGGACGAGGAGTTCCT 29
 1 TCGGACGAGGAGTTCCT 24

db 1 TCGGACGAGGAGTTCCT 24

RESULT 30
 AV947813 34 bp mRNA linear EST 17 MAR 2002
 LOCUS AV947813
 DEFINITION AV947813 North Satchu unpublished cDNA library, young adult Clona
 intestinalis cDNA clone cl1011045, mRNA sequence.
 ACCESSION AV947813
 VERSION AV947813.1 GI:1947022
 KEYWORDS EST.
 SOURCE Clona intestinalis
 ORGANISM Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euteleostomi,
 Phlebobranchia, Clonidae, Clona.


```

ACCESSION      AV966254
VERSION        AV966254.1
KEYWORDS       EST
SOURCE         GenBank
ORGANISM       Homo sapiens
REFERENCE      Salch, H., Salch, T., Kohn, T. and Salch, T.
              Expressed genes in Clona intestinalis
              (2000)
              Unpublished
              Contact: Nori Salch
              Department of Zoology
              University of
              Guelph, Ont. N1G 2W1, Canada
              Tel: 519-753-7531 ext 4001
              Fax: 519-753-7051 ext 1113
              Email: salch@uoguelph.ca and lyons@uoguelph.ca
              Location: Guelph, Ont.
AUTHORS        Salch, H., Salch, T., Kohn, T. and Salch, T.
TITLE          Expressed genes in Clona intestinalis
JOURNAL         Unpublished (2000)
COMMENT        Department of Zoology
              University of
              Guelph, Ont. N1G 2W1, Canada
              Tel: 519-753-7531 ext 4001
              Fax: 519-753-7051 ext 1113
              Email: salch@uoguelph.ca and lyons@uoguelph.ca
              Location: Guelph, Ont.

FEATURES             source
1..32
     /organism="Clona intestinalis"
     /db_xref="taxon:7923"
     /clone_lib="NCI9606"
     /clone_id="NCI9606.1"
     /cdiv="c1"
     /cdiv_type="whole animal"
     /seq_type="genomic"
     /note="Vector: pBluescript SK"

Query Match      42.7%; Score 12.9; PP 10; Length 32,
Best local similarity 70.9%; Prod. No. 36405;
Matches 17, Conservative 0, Miscellaneous 1, Indels 0, Gap 0
QY               6 TGGCGACGAGGAGATGTTCCT 29
Db               1 TTGGCGACGAGGATGTTCCTTTT 24

RESULT 22
AV966452        33 bp      TGA      linear      EST 14 MAR-2000
LOCUS          AV966452
DEFINITION    AV966452 Homo sapiens cDNA, complete cds, clone: 36405,
              International Human Genome Project (HGMP), GenBank,
              accession AV966452.1
VERSION        AV966452.1
KEYWORDS       EST
SOURCE         Clona intestinalis
ORGANISM       Clona intestinalis
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euteleostomi;
Phlebobranchia; Stolidobranchia
1 (bases 1 to 32)
Carch, H., Salch, T., Kohn, T. and Salch, T.
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Salch
Department of Zoology
University of
Guelph, Ont. N1G 2W1, Canada
Tel: 519-753-7531 ext 4001
Fax: 519-753-7051 ext 1113
Email: salch@uoguelph.ca and lyons@uoguelph.ca
Location: Guelph, Ont.

FEATURES             source
1..32
     /organism="Clona intestinalis"
     /db_xref="taxon:7923"
     /clone_lib="NCI9606"
     /clone_id="NCI9606.1"
     /cdiv="c1"
     /cdiv_type="whole animal"
     /seq_type="genomic"
     /note="Vector: pBluescript SK"

```

[illegible]

[illegible]

```

FEATURES
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHOR
TITLE
JOURNAL
COMMENT
Citation: 31-01018999
EST
Clona intestinalis.
Clona intestinalis.
Elkayama, M., Watanabe, C., Nakamura, T., Nishikawa, K., Akashi-Moriya, A.
Plebeletominae, Clonidae? Clona.
1 (bases 1 to 32)
Saitoh, Y., Saitoh, Y., Elkayama, T. and Shin-I, T.
Published online in Clon Intestinalis
Unpublished (2000)
Contact: Nori Satch
Department of Zoology
Kyoto University
Kyoto 606-8502, Japan
Tel: 81-75-753-4281
Fax: 81-75-753-1113
Email: satch@sci.kyoto-u.ac.jp.
Location/Qualifiers
1..32
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/cclone="cltb7k1"
/clone_lib="Nori Satch unpublished cDNA library"
/tissue_type="whole animal"
/dev_stage="adult"
Note "Genomic fingerprinting"
BASE COUNT
2 a 3 g 6 q 20 t
ORIGIN
Query Match 42.7% Contd.12.3 CF 10; Length 32
Best Local Similarity 70.8%; Pseq No 3e+05; % Incls 0; Size 0
Matches 1; Conservative 0; Mismatches 7;
Cy
6 TCGGACAGCAATGGTCTGT 29
||||| |||||
1 TTCCACAGCATTTTTTTT 24
DB
AV672108 32 bp RNA Library EST SE-01-001
LOCUS AV672108 32 bp RNA Library EST SE-01-001
DEFINITION AV672108 full length complementary DNA library from clonidial intestinalis
REMARKS cDNA clone seqtblast f, mRNA sequence.
ACCESSION AV672108
VERSION 1
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis.
ELKAYAMA, MARIKA, CHIKARA, TOSHIOHATA, AKASHI-MORIYA, EMORI, NORI
PLEBELETOMINA, CLONIDAE? Clona.
1 (bases 1 to 32)
Saitoh, Y., Saitoh, Y., Elkayama, T. and Shin I, T.
Unpublished paper in Clon Intestinalis
Unpublished (2000)
Contact: Nori Satch
Department of Zoology
Kyoto University
Kyoto 606-8502, Japan
Tel: 81-75-753-4281
Fax: 81-75-753-1113
Email: satch@sci.kyoto-u.ac.jp.
Location/Qualifiers
1..32
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/cclone="cltb7k1"
/clone_lib="Nori Satch unpublished cDNA library"
/tissue_type="whole animal"
/dev_stage="adult"
Note "Genomic fingerprinting"
FEATURES
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHOR
TITLE
JOURNAL
COMMENT

```


FEATURES
SOURCE
1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="cliv21k11"
/clone_lib="Nori Satoh unpublished cDNA library, larva"
/tissue_type="whole animal"
/dev_stage="tailbud"
/note="Vector: pGEMscript SK"

BASE COUNT
4 a 3 c 8 g 19 t

ORIGIN
Query Match 44.0% Score 13.2/ DB 10/ Length 34/
Best Local Similarity 69.2% Pred No. 2.1e+05/
Matches 18/ Conservative 0/ Mismatches 9/ Indels 0/ Gaps 0/
4 ATTCGGGCTGATGATTTCTCTT 29
2 AATTCGGGAGAGATTTCTCTT 29

RESULT 9
LOCUS
AV962582 34 bp cDNA linear EST 14-MAR-2002
DEFINITION
AV962582 Nori Satoh unpubl. cDNA library, larva cDNA
interstitials cDNA clone cliv21k11 5', mRNA sequence.
ACCESSION
AV962582.1 GI:19441842
VERSION
AV962582.1
KEYWORDS
SOURCE
ORGANISM
Clona intestinalis.
Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euteleostomi,
Pleurobranchia, Clariidae, Clona.
1 (bases 1 to 34)
Phlebotomus, Clariidae, Clona.
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo Ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohnori@zoology.kyoto-u.ac.jp

REFERENCE
AUTHORS
Satoh, N., Satoh, Y., Kohara, Y. and Shin, I.T.
TITLE
Expressed genes in Clona intestinalis
JOURNAL
Unpublished (2000)
COMMENT
Department of Zoology
Kyoto University
Sakyo Ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohnori@zoology.kyoto-u.ac.jp

BASE COUNT
4 a 3 c 8 g 20 t 1 others

ORIGIN
Query Match 44.0% Score 13.2/ DB 10/ Length 34/
Best Local Similarity 69.2% Pred No. 2.1e+05/
Matches 18/ Conservative 0/ Mismatches 9/ Indels 0/ Gaps 0/
4 ATTCGGGCTGATGATTTCTCTT 29
2 AATTCGGGAGAGATTTCTCTT 27

RESULT 10
LOCUS
AV962582 34 bp cDNA linear EST 14-MAR-2002
DEFINITION
AV962582 Nori Satoh unpubl. cDNA library, larva cDNA
interstitials cDNA clone cliv21k11 5', mRNA sequence.
ACCESSION
AV962582.1 GI:19441842
VERSION
AV962582.1
KEYWORDS
SOURCE
ORGANISM
Clona intestinalis.
Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euteleostomi,
Pleurobranchia, Clariidae, Clona.
1 (bases 1 to 34)
Phlebotomus, Clariidae, Clona.
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo Ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohnori@zoology.kyoto-u.ac.jp

REFERENCE
AUTHORS
Satoh, N., Satoh, Y., Kohara, Y. and Shin, I.T.
TITLE
Expressed genes in Clona intestinalis
JOURNAL
Unpublished (2000)
COMMENT
Department of Zoology
Kyoto University
Sakyo Ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohnori@zoology.kyoto-u.ac.jp

BASE COUNT
4 a 3 c 8 g 20 t 1 others

ORIGIN
Query Match 44.0% Score 13.2/ DB 10/ Length 34/
Best Local Similarity 69.2% Pred No. 2.1e+05/
Matches 18/ Conservative 0/ Mismatches 9/ Indels 0/ Gaps 0/
4 ATTCGGGCTGATGATTTCTCTT 29
2 AATTCGGGAGAGATTTCTCTT 27

RESULT 11
LOCUS
AV968830 35 bp cDNA linear EST 14-MAR-2002
DEFINITION
AV968830 Nori Satoh unpubl. cDNA library, larva cDNA
interstitials cDNA clone cliv21k11 5', mRNA sequence.
ACCESSION
AV968830
VERSION
AV968830.1 GI:19459594
KEYWORDS
SOURCE
ORGANISM
Clona intestinalis.
Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euteleostomi,
Pleurobranchia, Clariidae, Clona.
1 (bases 1 to 35)
Phlebotomus, Clariidae, Clona.
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo Ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohnori@zoology.kyoto-u.ac.jp

REFERENCE
AUTHORS
Satoh, N., Satoh, Y., Kohara, Y. and Shin, I.T.
TITLE
Expressed genes in Clona intestinalis
JOURNAL
Unpublished (2000)
COMMENT
Department of Zoology
Kyoto University
Sakyo Ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohnori@zoology.kyoto-u.ac.jp

BASE COUNT
1 a 3 c 8 g 20 t 1 others

ORIGIN
Query Match 44.0% Score 13.2/ DB 10/ Length 34/
Best Local Similarity 69.2% Pred No. 2.1e+05/
Matches 18/ Conservative 0/ Mismatches 9/ Indels 0/ Gaps 0/
4 ATTCGGGCTGATGATTTCTCTT 29
2 AATTCGGGAGAGATTTCTCTT 26

SOURCE
ORGANISM
Clona intestinalis.
Eukaryota, Metazoa, Chordata, Vertebrata, Actinoptera, Euteleostomi,
Pleurobranchia, Clariidae, Clona.
1 (bases 1 to 34)
Phlebotomus, Clariidae, Clona.
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo Ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satohnori@zoology.kyoto-u.ac.jp

FEATURES
SOURCE
1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="cliv21k11"
/clone_lib="Nori Satoh unpublished cDNA library, larva"
/tissue_type="whole animal"
/dev_stage="larva"
/note="Vector: pGEMscript SK"

BASE COUNT
1 a 3 c 8 g 20 t 1 others

ORIGIN
Query Match 44.0% Score 13.2/ DB 10/ Length 34/
Best Local Similarity 69.2% Pred No. 2.1e+05/
Matches 18/ Conservative 0/ Mismatches 9/ Indels 0/ Gaps 0/
4 ATTCGGGCTGATGATTTCTCTT 29
2 AATTCGGGAGAGATTTCTCTT 26

Query Match 44.0% Score 13.2 DB 9 Length 34
 Best Local Similarity 60.2% Pred Nov 2, 1995
 Matches 18 Conserved 9 Mismatches 9 Indels 0 Gaps 0

0Y 4 ATTGCGGACAGAGATTTTCTCT 23
 1 ATTTGCGGACAGAGATTTTCTCT 23

0B 4 ATTGCGGACAGAGATTTTCTCT 23
 1 ATTTGCGGACAGAGATTTTCTCT 23

RESULT 6
 AV658846 33 bp cDNA linear EST 14 MAR 2003
 LOCUS AV658846.1 GI:19447145
 DEFINITION intestinalis cDNA clone: cladi00657, mRNA sequence.
 VERSION AV658846.1 GI:19447145
 KEYWORDS EST
 SOURCE Clona intestinalis
 ORGANISM Clona intestinalis
 PHLEBOBRANCHIA: Cloniidae; Clona.
 1 (bases 1 to 33)
 Author: S. N. Saitoh, Y. Fukui, Y. and Shun-ichi
 Title: Expressed genes in Clona intestinalis
 Journal: Unpublished (2000)
 Comment: Contact: Nori Saitoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto 606-8501 Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: saichiro@kaiyodai.kyoto-u.ac.jp

FEATURES
 source
 1..33
 /organism="Clona intestinalis"
 /db_xref="taxon:7719"
 /clone="cladi00657"
 /locus_tag="19447145" /published="Clona library, young adult"

BASE COUNT
 4 a 4 c 13 g 17 t

ORIGIN
 Query Match 44.0% Score 13.2 DB 9 Length 33
 Best Local Similarity 60.2% Pred Nov 2, 1995
 Matches 18 Conserved 9 Mismatches 9 Indels 0 Gaps 0

0Y 4 ATTGCGGACAGAGATTTTCTCT 23
 1 ATTTGCGGACAGAGATTTTCTCT 23

0B 4 ATTGCGGACAGAGATTTTCTCT 23
 1 ATTTGCGGACAGAGATTTTCTCT 23

RESULT 7
 A1446718 34 bp cDNA linear EST 06 MAR 1999
 LOCUS A1446718.1 GI:19447145
 DEFINITION intestinalis cDNA clone: cladi00657, mRNA sequence.
 VERSION A1446718.1 GI:19447145
 KEYWORDS EST
 SOURCE Clona intestinalis
 ORGANISM Clona intestinalis
 PHLEBOBRANCHIA: Cloniidae; Clona.
 1 (bases 1 to 34)
 Author: S. N. Saitoh, Y. Fukui, Y. and Shun-ichi
 Title: Expressed genes in Clona intestinalis
 Journal: Unpublished (2000)
 Comment: Contact: Nori Saitoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto 606-8501 Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: saichiro@kaiyodai.kyoto-u.ac.jp

Query Match 44.0% Score 13.2 DB 9 Length 34
 Best Local Similarity 60.2% Pred Nov 2, 1995
 Matches 18 Conserved 9 Mismatches 9 Indels 0 Gaps 0

0Y 5 TTGCGGACAGAGATTTTCTCT 30
 1 TTTGCGGACAGAGATTTTCTCT 30

0B 31 TTGCGGACAGAGATTTTCTCT 30
 1 TTTGCGGACAGAGATTTTCTCT 30

RESULT 8
 AV675869 34 bp cDNA linear EST 06 MAR 2003
 LOCUS AV675869.1 GI:19447145
 DEFINITION intestinalis cDNA clone: cladi00657, mRNA sequence.
 VERSION AV675869.1 GI:19447145
 KEYWORDS EST
 SOURCE Clona intestinalis
 ORGANISM Clona intestinalis
 PHLEBOBRANCHIA: Cloniidae; Clona.
 1 (bases 1 to 34)
 Author: S. N. Saitoh, Y. Fukui, Y. and Shun-ichi
 Title: Expressed genes in Clona intestinalis
 Journal: Unpublished (2000)
 Comment: Contact: Nori Saitoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto 606-8501 Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: saichiro@kaiyodai.kyoto-u.ac.jp

Trace considered overall poor quality
 Set primer: -40bp from Gibco
 High quality sequence: 1.
 Location/Qualifiers
 1..34
 /organism="Clona intestinalis"
 /db_xref="taxon:7719"
 /clone="cladi00657"
 /locus_tag="19447145" /published="Clona library, young adult"

BASE COUNT
 9 a 10 c 13 g 2 t

ORIGIN
 Query Match 44.0% Score 13.2 DB 9 Length 34
 Best Local Similarity 60.2% Pred Nov 2, 1995
 Matches 18 Conserved 9 Mismatches 9 Indels 0 Gaps 0

0Y 5 TTGCGGACAGAGATTTTCTCT 30
 1 TTTGCGGACAGAGATTTTCTCT 30

0B 31 TTGCGGACAGAGATTTTCTCT 30
 1 TTTGCGGACAGAGATTTTCTCT 30

RESULT 9
 AV675869 34 bp cDNA linear EST 06 MAR 2003
 LOCUS AV675869.1 GI:19447145
 DEFINITION intestinalis cDNA clone: cladi00657, mRNA sequence.
 VERSION AV675869.1 GI:19447145
 KEYWORDS EST
 SOURCE Clona intestinalis
 ORGANISM Clona intestinalis
 PHLEBOBRANCHIA: Cloniidae; Clona.
 1 (bases 1 to 34)
 Author: S. N. Saitoh, Y. Fukui, Y. and Shun-ichi
 Title: Expressed genes in Clona intestinalis
 Journal: Unpublished (2000)
 Comment: Contact: Nori Saitoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto 606-8501 Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: saichiro@kaiyodai.kyoto-u.ac.jp

RECEIVED
ORIGIN

QY 10 GCAGAGGAAITGTTCTGT 29
 ||| ||| ||| ||| |||
 TB 12 GCACAAGGAGTTGTTTGT 31

ACCESSION AV672830
 DEPOSITION 22.07.1997
 NUMBER AV672830.1
 KEYWORDS EST,
 SOURCE *Ciona intestinalis*,
 ORGANISM *Ciona intestinalis*

Department of Zoology
University of
Sakyo Ku, Kyoto, Japan
Tel: 81-75-753-4081

```

logname="core"
db_xref="350000000"
format="pvc"
format="pvc"

```

[illegible]

oy 4 ATTGGGCGAGGACAAATTTCTTTCCT 29
| | ||||| | | | |
zb 2 AATTGGGACGAAGGTCTTTTCTTTT 27

RESULT 4

```
source      1. .31
            /organism: "Clona intestinalis"
            /db_xref="taxon:7719"
```

Early March	44.0°	Green 17.77	Ln 10	Length 31
Peak local similarity	69.2%	Prod. No. 26405		
March 16, 1968	44.0°	Green 17.77	Ln 10	Length 31

LOCUS	P03936	22 bp	mRNA	1100 nt
DEFINITION	Protein M18-1 protein, Homo sapiens, HBBPUS			
FEATURES	Note: some data indicate that RNA sequence.			
ACCESSION	B003982			

[illegible]

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
mol.gen@mol.gen.ri.go.jp

Email: techinfo@cs.mcgill.ca
 Location: cs.mcgill.ca/~iliev
 1. .32
 source

[illegible]

ALIGNMENTS

RESULT 1
R0064029 44 bp MRNA linear EST 07 DEC 2001
DEFINITION
LOCUS
R0064029
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

R0064029 44 bp MRNA linear EST 07 DEC 2001
R0064029 R0064029
laevis cDNA clone K126007-07, RNA sequence.
R0064029
R0064029 1 nt 1242067
EST
African clawed frog.
Xenopus laevis
Fukuyama, Morita, Choudhry, Gnanaprakasam, Vetrabalan, Erelalossami,
Amphibian; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus
1 (bases 1 to 34)
Kiyama, Toriizawa, Yoshida, Nakai, Shimizu and Shibata
y.
Expressed from a X. laevis cDNA
unpublished (2001)
Contact: Tadashi Shimizu

Prepared under the X-ray and by
Unpublished (2001)
Contact: Tadasu Shin-
i
National Institute of Science and Technology
1-1-1 Higashi, Tsukuba, Shizuoka 411-8540, Japan
Tel: 81-559 81 6856

FAX: 01 509 81 6855
 Email: skindjones@jag.jp
 Tel: 01 509 81 6855
 1. 24

FACE
ORIGIN

Clery, M. G.
Best Local
Matches

15

5 GGNAAATTCGGCAGGAGGTTT TTTT TTTT 33

A2470637

SECRET
REF ID: A66110

AS ITWCS

SAFETY

TITLE

JOURNAL
COMMENT

FRATIPES

SOURCE

Location/Qualifiers
1. .34

"Yes, I'm a Jew."

COIN THE "NATIVE" FOR

1. *Chlorophyll a* (Chl a) and *Chlorophyll b* (Chl b) are the two main photosynthetic pigments in green plants. They are responsible for capturing light energy and converting it into chemical energy through the process of photosynthesis.

[illegible]

musculus C57BL/6J (ma

10) was obtained from the Takara

— 100 —

100

1

[illegible]

226	10.2	34.0	30	17	AD71602	AD71602	IM04581	AD71602	IM04581
227	10.2	34.0	30	17	AD71603	AD71603	IM04582	AD71603	IM04582
228	10.2	34.0	30	17	AD71604	AD71604	IM04583	AD71604	IM04583
229	10.2	34.0	30	17	AD71605	AD71605	IM04584	AD71605	IM04584
230	10.2	34.0	30	17	AD71606	AD71606	IM04585	AD71606	IM04585
231	10.2	34.0	30	17	AD71607	AD71607	IM04586	AD71607	IM04586
232	10.2	34.0	30	17	AD71608	AD71608	IM04587	AD71608	IM04587
233	10.2	34.0	30	17	AD71609	AD71609	IM04588	AD71609	IM04588
234	10.2	34.0	30	17	AD71610	AD71610	IM04589	AD71610	IM04589
235	10.2	34.0	30	17	AD71611	AD71611	IM04590	AD71611	IM04590
236	10.2	34.0	30	17	AD71612	AD71612	IM04591	AD71612	IM04591
237	10.2	34.0	30	17	AD71613	AD71613	IM04592	AD71613	IM04592
238	10.2	34.0	30	17	AD71614	AD71614	IM04593	AD71614	IM04593
239	10.2	34.0	30	17	AD71615	AD71615	IM04594	AD71615	IM04594
240	10.2	34.0	30	17	AD71616	AD71616	IM04595	AD71616	IM04595
241	10.2	34.0	30	17	AD71617	AD71617	IM04596	AD71617	IM04596
242	10.2	34.0	30	17	AD71618	AD71618	IM04597	AD71618	IM04597
243	10.2	34.0	30	17	AD71619	AD71619	IM04598	AD71619	IM04598
244	10.2	34.0	30	17	AD71620	AD71620	IM04599	AD71620	IM04599
245	10.2	34.0	30	17	AD71621	AD71621	IM04600	AD71621	IM04600
246	10.2	34.0	30	17	AD71622	AD71622	IM04601	AD71622	IM04601
247	10.2	34.0	30	17	AD71623	AD71623	IM04602	AD71623	IM04602
248	10.2	34.0	30	17	AD71624	AD71624	IM04603	AD71624	IM04603
249	10.2	34.0	30	17	AD71625	AD71625	IM04604	AD71625	IM04604
250	10.2	34.0	30	17	AD71626	AD71626	IM04605	AD71626	IM04605
251	10.2	34.0	30	17	AD71627	AD71627	IM04606	AD71627	IM04606
252	10.2	34.0	30	17	AD71628	AD71628	IM04607	AD71628	IM04607
253	10.2	34.0	30	17	AD71629	AD71629	IM04608	AD71629	IM04608
254	10.2	34.0	30	17	AD71630	AD71630	IM04609	AD71630	IM04609
255	10.2	34.0	30	17	AD71631	AD71631	IM04610	AD71631	IM04610
256	10.2	34.0	30	17	AD71632	AD71632	IM04611	AD71632	IM04611
257	10.2	34.0	30	17	AD71633	AD71633	IM04612	AD71633	IM04612
258	10.2	34.0	30	17	AD71634	AD71634	IM04613	AD71634	IM04613
259	10.2	34.0	30	17	AD71635	AD71635	IM04614	AD71635	IM04614
260	10.2	34.0	30	17	AD71636	AD71636	IM04615	AD71636	IM04615
261	10.2	34.0	30	17	AD71637	AD71637	IM04616	AD71637	IM04616
262	10.2	34.0	30	17	AD71638	AD71638	IM04617	AD71638	IM04617
263	10.2	34.0	30	17	AD71639	AD71639	IM04618	AD71639	IM04618
264	10.2	34.0	30	17	AD71640	AD71640	IM04619	AD71640	IM04619
265	10.2	34.0	30	17	AD71641	AD71641	IM04620	AD71641	IM04620
266	10.2	34.0	30	17	AD71642	AD71642	IM04621	AD71642	IM04621
267	10.2	34.0	30	17	AD71643	AD71643	IM04622	AD71643	IM04622
268	10.2	34.0	30	17	AD71644	AD71644	IM04623	AD71644	IM04623
269	10.2	34.0	30	17	AD71645	AD71645	IM04624	AD71645	IM04624
270	10.2	34.0	30	17	AD71646	AD71646	IM04625	AD71646	IM04625
271	10.2	34.0	30	17	AD71647	AD71647	IM04626	AD71647	IM04626
272	10.2	34.0	30	17	AD71648	AD71648	IM04627	AD71648	IM04627
273	10.2	34.0	30	17	AD71649	AD71649	IM04628	AD71649	IM04628
274	10.2	34.0	30	17	AD71650	AD71650	IM04629	AD71650	IM04629
275	10.2	34.0	30	17	AD71651	AD71651	IM04630	AD71651	IM04630
276	10.2	34.0	30	17	AD71652	AD71652	IM04631	AD71652	IM04631
277	10.2	34.0	30	17	AD71653	AD71653	IM04632	AD71653	IM04632
278	10.2	34.0	30	17	AD71654	AD71654	IM04633	AD71654	IM04633
279	10.2	34.0	30	17	AD71655	AD71655	IM04634	AD71655	IM04634
280	10.2	34.0	30	17	AD71656	AD71656	IM04635	AD71656	IM04635
281	10.2	34.0	30	17	AD71657	AD71657	IM04636	AD71657	IM04636
282	10.2	34.0	30	17	AD71658	AD71658	IM04637	AD71658	IM04637
283	10.2	34.0	30	17	AD71659	AD71659	IM04638	AD71659	IM04638
284	10.2	34.0	30	17	AD71660	AD71660	IM04639	AD71660	IM04639
285	10.2	34.0	30	17	AD71661	AD71661	IM04640	AD71661	IM04640
286	10.2	34.0	30	17	AD71662	AD71662	IM04641	AD71662	IM04641
287	10.2	34.0	30	17	AD71663	AD71663	IM04642	AD71663	IM04642
288	10.2	34.0	30	17	AD71664	AD71664	IM04643	AD71664	IM04643
289	10.2	34.0	30	17	AD71665	AD71665	IM04644	AD71665	IM04644
290	10.2	34.0	30	17	AD71666	AD71666	IM04645	AD71666	IM04645
291	10.2	34.0	30	17	AD71667	AD71667	IM04646	AD71667	IM04646
292	10.2	34.0	30	17	AD71668	AD71668	IM04647	AD71668	IM04647
293	10.2	34.0	30	17	AD71669	AD71669	IM04648	AD71669	IM04648
294	10.2	34.0	30	17	AD71670	AD71670	IM04649	AD71670	IM04649
295	10.2	34.0	30	17	AD71671	AD71671	IM04650	AD71671	IM04650
296	10.2	34.0	30	17	AD71672	AD71672	IM04651	AD71672	IM04651
297	10.2	34.0	30	17	AD71673	AD71673	IM04652	AD71673	IM04652
298	10.2	34.0	30	17	AD71674	AD71674	IM04653	AD71674	IM04653

Publication No. US2003068723A1
GENERAL INFORMATION:
APPLICANT: Daikee, Shanz H.
TITLE OF INVENTION: PROGNOSTIC METHOD FOR BREAST CANCER
FILE REFERENCE: CMC 016/0095
CURRENT APPLICATION NUMBER: US/09/416,460C
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patent In version 3.1
SEQ ID NO 44
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic primer
US 09 816 460C 44

Query Match 44 04: Score 13.2; 5P 12; Length 20;
Best local similarity 83.34, Fred. No. 1.9e+04;
Matches 15, Conservative 57, Mismatches 3, Indels 0, Gaps 0;

CY 10 GAGAGAGAAATTTTCT 27
|||||
DB 20 GAGAGAGAAATTTCT 3

Search completed: July 21, 2003, 18:30:13
Job time : 83.6397 secs

APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/02/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 66020
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-66020

Query Match 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity 73.9%, Freq. No. 1,66+04,
 Matches 17, Conservative 0, Mismatches 6, Indels 0, Pairs 0

QY 5 TTGGGAGAGAGAGATGTTGT 27
 DB 24 TCGGAGAGAGAGCTCTGTGT 2

RESULT 36
 US-10-098-263B-78475/C
 Sequence 78475, Application US/02/098,263B
 Publication No. US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/02/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 78475
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-78475

Query Match 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity 73.9%, Freq. No. 1,66+04,
 Matches 17, Conservative 0, Mismatches 6, Indels 0, Pairs 0

QY 8 GGGCAGAGAGATGTTGTGT 30
 DB 24 GGGAGAGAGAGATGTTGT 2

RESULT 37
 US-10-098-263B-11071/C
 Sequence 11071, Application US/02/098,263B
 Publication No. US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/02/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 11071
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-11071

Query Match 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity 73.9%, Freq. No. 1,66+04,
 Matches 17, Conservative 0, Mismatches 6, Indels 0, Pairs 0

QY 1 GAAATGGAGAGAGATGTTGT 23
 DB 23 GAAATGGAGAGAGATGTTGT 1

RESULT 38
 US-10-098-263B-11072/C
 Sequence 11072, Application US/02/098,263B
 Publication No. US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/02/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 11072
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-11072

Query Match 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity 73.9%, Freq. No. 1,66+04,
 Matches 17, Conservative 0, Mismatches 6, Indels 0, Pairs 0

QY 1 GAAATGGAGAGAGATGTTGT 23
 DB 23 GAAATGGAGAGAGATGTTGT 1

RESULT 39
 US-10-131-175-16/C
 Sequence 10, Application US/01/031,175
 Publication No. US20030104417A1
 GENERAL INFORMATION:
 APPLICANT: Dupret, Daniel
 AFFILIANT: Masson, Jean-Michel
 TITLE OF INVENTION: Polynucleotides
 FILE REFERENCE: 58/063,000/21
 CURRENT APPLICATION NUMBER: US/01/031,175
 CURRENT FILING DATE: 2002-08-07
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 10
 LENGTH: 28
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthesized antisense primer
 US-10-131-175-10

Query Match 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity 93.8%, Freq. No. 1,66+04,
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Pairs 0

QY 1 GGGCAGAGAGATGTTGT 21
 DB 17 GGGCAGAGAGATGTTGT 3

RESULT 40
 US-09-816-460C-44/C
 Sequence 44, Application US/098,6460C

[illegible]

US-10-205-009-63

Query Match 46.0% Score 13.8; DB 15; Length 28;
 Best Local Similarity 70.6%; Pred. No. 1,1e+04;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 TGGGCGAGGAGGAAATTT 22

2b 6 TGGGCGAGGAGGAAATTT 22

RESULT 21

US-10-205-009-61

Sequence 61, Application US/10205009
 Publication No. US2000114404A1
 GENERAL INFORMATION
 APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMITT, CHANIFA
 APPLICANT: VARGHESE
 APPLICANT: MICHAEL WILLIS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NUCLEIC
 ACID SEQUENCES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Fremont Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10205009

FILING DATE: 21 JULY 2002

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/014,968

FILING DATE: 13 Mar 2000

APPLICATION NUMBER: EC/03/7/19344

FILING DATE: 17 OCTOBER 1997

APPLICATION NUMBER: 08/733,109

FILING DATE: 26 OCTOBER 1996

APPLICATION NUMBER: 08/970,930

FILING DATE: 6 JUNE 1997

APPLICATION NUMBER: 08/970,930

FILING DATE: 21 JULY 1997

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,415

REFERENCE/EXCERPT NUMBER: 33,415/0007 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2' thio modified

US-10-205-009-61

Query Match 46.0% Score 13.8; DB 15; Length 28;
 Best Local Similarity 70.6%; Pred. No. 1,1e+04;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 TGGGCGAGGAGGAAATTT 22

2b 6 TGGGCGAGGAGGAAATTT 22

RESULT 22

US-10-205-009-78

Sequence 78, Application US/10205009
 Publication No. US2000114404A1
 GENERAL INFORMATION
 APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMITT, CHANIFA
 APPLICANT: VARGHESE
 APPLICANT: MICHAEL WILLIS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NUCLEIC
 ACID SEQUENCES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Fremont Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10205009

FILING DATE: 25 JULY 2002

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/014,968

FILING DATE: 13 Mar 2000

APPLICATION NUMBER: EC/03/7/19344

FILING DATE: 17 OCTOBER 1997

APPLICATION NUMBER: 08/733,109

FILING DATE: 26 OCTOBER 1996

APPLICATION NUMBER: 08/970,930

FILING DATE: 6 JUNE 1997

APPLICATION NUMBER: 08/970,930

FILING DATE: 21 JULY 1997

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,415

REFERENCE/EXCERPT NUMBER: 33,415/0007 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 29

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2' thio modified

OTHER INFORMATION: Purines are 2' (methyl) (2'-Me) modified

OTHER INFORMATION: Purines are 2' (methyl) (2'-Me) modified

OTHER INFORMATION: Purines are 2' (methyl) (2'-Me) modified

US-10-205-009-78

Query Match 46.0% Score 13.8; DB 15; Length 28;
 Best Local Similarity 70.6%; Pred. No. 1,1e+04;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

LENGTH: 22
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: PCR Primer
 US-09-066-158 4

Query Match 46.7%, Score 14, E=12, Length 22
 Best Local Similarity 77.3%, Pred. No. 8.6e+03
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

US-09-066-158 4
 3 ATTGCGGAGGAGATTTGTTG 24
 22 AGTGGGAGGAGATTTGTTG 1

RESULT 18
 US-09-863-830-137/C

Sequence 137, Application US/09853830
 Patent No. US2002010188A1

GENERAL INFORMATION:
 APPLICANT: Vardach, Arthur A.
 TITLE OF INVENTION: Methods of Identifying and Modulating
 TIME OF INVENTION: 1998-01-01
 FILE REFERENCE: P-10 4794

CURRENT AFFILIATION NUMBER: 12/10/2002
 CURRENT FILING DATE: 2001-09-18
 NUMBER OF SEQ ID NOS: 184

SOFTWARE: FASTCG for Windows Version 1.0
 SEQ ID NO: 137

LENGTH: 24
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-863-830-137

Query Match 46.7%, Score 14, E=12, Length 24
 Best Local Similarity 77.3%, Pred. No. 8.7e+03
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

US-09-863-830-137
 7 GCGGAGGAGGATTTGTTG 28
 22 GCGGAGGAGGATTTGTTG 1

RESULT 19
 US-10-095-672A-74/C

Sequence 137, Application US/09853830
 Patent No. US2002010188A1

GENERAL INFORMATION:
 APPLICANT: Herd, Thelma
 APPLICANT: Thelma, Thelma
 APPLICANT: Roman-Roman, Sergio

APPLICANT: Roman-Roman, Sergio
 TITLE OF INVENTION: Methods of Identifying and Modulating
 TIME OF INVENTION: 1998-01-01
 FILE REFERENCE: P-10 4794

CURRENT AFFILIATION NUMBER: 12/10/2002
 CURRENT FILING DATE: 2002-03-12
 NUMBER OF SEQ ID NOS: 184

SOFTWARE: FASTCG for Windows Version 1.0
 SEQ ID NO: 137

LENGTH: 24
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-095-672A-74/C

Query Match 46.7%, Score 14, E=12, Length 24
 Best Local Similarity 77.3%, Pred. No. 8.7e+03
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

SEQ ID NO 74
 LENGTH: 24
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Type V Alpha 13
 US-10-095-672A-74

Query Match 46.7%, Score 14, E=12, Length 24
 Best Local Similarity 77.3%, Pred. No. 8.7e+03
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

US-10-095-672A-74
 7 GCGGAGGAGGATTTGTTG 24
 22 GCGGAGGAGGATTTGTTG 1

RESULT 20
 US-10-205-009-60

Sequence 137, Application US/10200960
 Patent No. US2002010188A1

GENERAL INFORMATION:
 APPLICANT: Vardach, Arthur A.
 TITLE OF INVENTION: Methods of Identifying and Modulating
 TIME OF INVENTION: 1998-01-01
 FILE REFERENCE: P-10 4794

CURRENT AFFILIATION NUMBER: 12/10/2002
 CURRENT FILING DATE: 2001-09-18
 NUMBER OF SEQ ID NOS: 184

SOFTWARE: FASTCG for Windows Version 1.0
 SEQ ID NO: 137

LENGTH: 24
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-205-009-60

Query Match 46.7%, Score 14, E=12, Length 24
 Best Local Similarity 77.3%, Pred. No. 8.7e+03
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

US-10-205-009-60
 7 GCGGAGGAGGATTTGTTG 28
 22 GCGGAGGAGGATTTGTTG 1

RESULT 21
 US-10-205-009-60

Sequence 137, Application US/10200960
 Patent No. US2002010188A1

GENERAL INFORMATION:
 APPLICANT: Vardach, Arthur A.
 TITLE OF INVENTION: Methods of Identifying and Modulating
 TIME OF INVENTION: 1998-01-01
 FILE REFERENCE: P-10 4794

CURRENT AFFILIATION NUMBER: 12/10/2002
 CURRENT FILING DATE: 2001-09-18
 NUMBER OF SEQ ID NOS: 184

SOFTWARE: FASTCG for Windows Version 1.0
 SEQ ID NO: 137

LENGTH: 24
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-205-009-60

Query Match 46.7%, Score 14, E=12, Length 24
 Best Local Similarity 77.3%, Pred. No. 8.7e+03
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

US-10-205-009-60
 7 GCGGAGGAGGATTTGTTG 28
 22 GCGGAGGAGGATTTGTTG 1

RESULT 14
US-10-060-830 537
Sequence 537, Application US/006691
Publication No. US20030315441
GENERAL INFORMATION:
APPLICANT: Nguyen, Dung Thuan
TITLE OF INVENTION: RNAI FOR Tumor Treatment (2001-01-30)
FILE REFERENCE: 000000
CURRENT APPLICATION NUMBER: US/09/060,830
CURRENT FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US/01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US/01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US/01/00662
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 1123
SOFTWARE: Assembla Sequence Listing Engine
SEQ ID NO 536
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-060-830 536

Query Match 48.0%, Score 14.4, DB 15, Length 25;
Best Local Similarity 93.8%, Freq. No. 5, 9e+03;
Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0

CY 9 GAGAGAGAGATGTT 24
DB 2 GATAGAGAGATGTT 17

RESULT 14
US-10-060-830 537
Sequence 537, Application US/006691
Publication No. US20030315441
GENERAL INFORMATION:
APPLICANT: Nguyen, Dung Thuan
TITLE OF INVENTION: RNAI FOR Tumor Treatment (2001-01-30)
FILE REFERENCE: 000000
CURRENT APPLICATION NUMBER: US/09/060,830
CURRENT FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US/01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US/01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US/01/00662
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 1123
SOFTWARE: Assembla Sequence Listing Engine
SEQ ID NO 537
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-060-830 537

Query Match 48.0%, Score 14.4, DB 15, Length 25;
Best Local Similarity 93.8%, Freq. No. 5, 9e+03;
Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0

CY 9 GAGAGAGAGATGTT 24
DB 1 GATAGAGAGATGTT 16

RESULT 15
US-10-215-112 9292/c
Sequence 9292, Application US/00215112
Publication No. US2003078217A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Gene Expression of Proteins
FILE REFERENCE: 0119
CURRENT APPLICATION NUMBER: US/02/015,112
CURRENT FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 14916
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9292
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112 9292

Query Match 48.0%, Score 14.4, DB 15, Length 25;
Best Local Similarity 93.8%, Freq. No. 3e+03;
Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0

CY 3 AATGCGCGAGAGGA 18
DB 22 AATGCGCGAGAGGA 7

RESULT 16
US-10-215-112-13271/c
Sequence 13271, Application US/00215112
Publication No. US200308206A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Gene Expression of Proteins
FILE REFERENCE: 0119
CURRENT APPLICATION NUMBER: US/02/015,112
CURRENT FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 14916
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13271
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-13271

Query Match 48.0%, Score 14.4, DB 15, Length 25;
Best Local Similarity 93.8%, Freq. No. 5, 9e+03;
Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0

CY 3 AATGCGCGAGAGGA 18
DB 23 AATGCGCGAGAGGA 8

RESULT 17
US-09-906-158-4/c
Sequence 4, Application US/0906158
Publication No. US2003078217A1
GENERAL INFORMATION:
APPLICANT: Brett E. Moulis
TITLE OF INVENTION: ARTISERNE MODIFICATION OF TRANSFER RNA
FILE REFERENCE: RTS-0257
CURRENT APPLICATION NUMBER: US/09/096,158
CURRENT FILING DATE: 2001-07-14
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 4

Query Match 48.0%, Score 14.4, DB 15, Length 25;
Best Local Similarity 93.8%, Freq. No. 5, 9e+03;
Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-1000
TELEFAX: (212) 953-7249
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide DNA
US-08-353-761-14

Query Match 43.3%; Score 13; DB 1; Length 30;

Best Local Similarity 76.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

9 GGCACGAGGATGTTCTCT 29
|||||||
3D 9 GGCACGATCGAGCTTCACT 29

Search completed: July 21, 2003, 15:48:55
Job time: 30.994 secs

APPLICANT: CHUNG, Dong Hyun.
 APPLICANT: NAM, Soo Man.
 APPLICANT: KIM, Byung Moon.
 APPLICANT: KANG, Guk Ah.
 APPLICANT: PARK, Young Moon.
 TITLE OF INVENTION: SIGNAL SEQUENCES FOR SECRETION
 TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS FROM
 TITLE OF INVENTION: YEAST
 NUMBER OF SEQUENCES: 23
 CORRESPONDENT ADDRESS
 ADDRESSEE: CHUNG, Dong Hyun
 STREET: Hanwool Apt. 101-702, Shinsung-dong,
 STREET: Yuseong-gu
 CITY: Daejeon
 STATE:
 COUNTRY: Republic of Korea
 ZIP: 305-345
 ADDRESSEE: NAM, Soo Man
 STREET: Hanwool Apt. 101-705, 23, Guk-dong,
 STREET: Yuseong-gu
 CITY: Daejeon
 STATE:
 COUNTRY: Republic of Korea
 ZIP: 305-333
 ADDRESSEE: KIM, Byung Moon
 STREET: 53-2, Beokseong-dong
 CITY: Cheongju-si
 STATE: Chungcheongbuk-do
 COUNTRY: Republic of Korea
 ZIP: 360-270
 ADDRESSEE: YANG, Sun Ah
 STREET: 606-10, Shincheon-1-dong,
 STREET: Dong-gu
 CITY: Daejeon
 STATE:
 COUNTRY: Republic of Korea
 ZIP: 701-021
 ADDRESSEE: PARK, Young Moon
 STREET: Town House 1-101, 101, Gyeongju-buk,
 STREET: Yuseong-gu
 CITY: Daejeon
 STATE:
 COUNTRY: Republic of Korea
 ZIP: 305-340
 COMPUTER READABLE FORM:
 MEDIA TYPE: Diskette, 5.25inch, 1.44M Storage
 COMPUTER: IBM PC/AT
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 2000-00000000-0000
 FILING DATE: 12-DEC-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: KR 93 27265
 FILING DATE: 10-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Shahan, Islam
 REGISTRATION NUMBER: 32,137
 REFERENCE/DOCUMENT NUMBER: A 0683
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-1000
 TELEFAX: (212) 252-7319
 INFORMATION FEE: \$25.00
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: oligonucleotide, DNA
 05-08-2013-75119

```

07          9  GATTACAAGATGTTCTTTC 29
DB      68  GGCAAGAAGCAGACGCGAATTAAGT 8

RESULT 40
Sequence ID: 551-14
Patent No.: 5712113
GENERAL INFORMATION:
APPLICANT: CHUNG, Bong Hyun
APPLICANT: NAM, Soo Wan
APPLICANT: KIM, Byung Moon
APPLICANT: YANG, Sun Ah
TITLE OF INVENTION: SIGNAL SEQUENCE FOR SECRETION
TITLE OF INVENTION: OF HYPOTHETICAL PROTEINS FROM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: CHUNG, Bong Hyun
STREET: Hakdang Apt. 1st floor, Chilsung-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-345
ADDRESSER: NAM, Soo Wan
STREET: Hadit Apt. 1st floor, 2nd, out-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-333
ADDRESSER: KIM, Byung Moon
STREET: 51 E, Boksae-dong
CITY: Cheongju-si
SALAH: Chungcheongbuk-do
COUNTRY: Republic of Korea
ZIP: 360-270
ADDRESSER: YANG, Sun Ah
STREET: 626-10, Shincheon 1-dong,
STREET: Dong-gu
CITY: Daegu
STATE:
COUNTRY: Republic of Korea
ZIP: 701-021
ALLIANCE NAME: Yang-Huh
STREET: Town House S-131, 391, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-340
COMPILED READABLE FORM:
METHOD TITLE: Database, English, LGH storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect 5.1
CURRENT AFFILIATION DATA:
AFFILIATION NUMBER: 0066/553,751
FILING DATE: 12-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 94-07269
FILING DATE: 10-DEC-1993
AGENT/ASNT INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER: 32,507
REFERENCE/SECRET NUMBER: A 9903
```


2b 2 GAAATTCGAGCTGAGACTT 22

RESULT 17

US-08-220-606B-R

Sequence 9, Affiliation: US/08157751

Patent No. 641661

GENERAL INFORMATION:

APPLICANT: Kumagai, Monto H.

APPLICANT: Genadi, Swerlow J.

TITLE OF INVENTION: RICHIA POLYMER AS A CELLULOSE CELLULOSE AND

TITLE OF INVENTION: RICHIA POLYMER AS A CELLULOSE CELLULOSE AND

NUMBER OF INVENTION: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Fasta 2.9 Release #1.0, Version #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/157751

FILING DATE: 25-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 16,427

REFERENCE/AGENT INFORMATION:

TELEPHONE: 415-854-3660

TELEFAX: 415-854-3664

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA

US-08-220-606B-R

Query Match 43.3% Score 13 DB 1, Length 30

Best Local Similarity 76.2% Freq. No. 2,56,03

Matches 16, Conservative 0, Mismatches 0, Indels 0

2y 4 ATTGATTCGAGCTGAGACTT 24

2b 2 AATGATTCGAGCTGAGACTT 22

RESULT 38

US-08-353-751-R

Sequence 8, Affiliation: US/08157751

Patent No. 5712113

GENERAL INFORMATION:

APPLICANT: CHUNG, Peng Hyun

APPLICANT: NAM, Soo Wan

APPLICANT: KIM, Byung Moon

APPLICANT: YANG, Sun Ah

APPLICANT: PARK, Young Hoon

TITLE OF INVENTION: STABLE SEQUENCES FOR CELLULAR

TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS FROM

NUMBER OF INVENTION: 23

ADDRESSEE: CHUNG, Peng Hyun

STREET: Harvard Apt. 101-102, Chinsung Jang,

STREET: Yuseong 91

CITY: Daejeon

STATE:

COUNTRY: Republic of Korea

ZIP: 305-345

ADDRESSEE: NAM, Soo Wan

STREET: Hanbit Apt. 111-105, 91, Chinsung Jang,

STREET: Yuseong-gu

CITY: Daejeon

STATE:

COUNTRY: Republic of Korea

ZIP: 305-343

ADDRESSEE: KIM, Byung Moon

STREET: 53-2, Beksae-dong

CITY: Cheongju-si

STATE: Chungcheongbuk-do

COUNTRY: Republic of Korea

ZIP: 360-270

ADDRESSEE: YANG, Sun Ah

STREET: 626-13, Shinscheon 1-dong,

STREET: Dong-gu

CITY: Daejeon

STATE:

COUNTRY: Republic of Korea

ZIP: 701-021

ADDRESSEE: JAFY, Young Hoon

STREET: Town House S 101, 351, Doyong-dong,

STREET: Yuseong-gu

CITY: Daejeon

STATE:

COUNTRY: Republic of Korea

ZIP: 305-340

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 1.2MB Storage

COMPUTER: IBM PC/AT

OPERATING SYSTEM: MS-DOS

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,751

FILING DATE: 12-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: KR 93 07073

FILING DATE: 10 DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Shaheen Islam

REGISTRATION NUMBER: 32,597

REFERENCE/AGENT NUMBER: A 0003

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 953-7249

TELEFAX: (212) 953-7249

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: oligonucleotide DNA

US-08-353-751-R

Query Match 43.3% Score 13 DB 1, Length 30

Best Local Similarity 76.2% Freq. No. 2,56,03

Matches 16, Conservative 0, Mismatches 0, Indels 0

2y 9 GATGATTCGAGCTGAGACTT 29

2b 9 GATGATTCGAGCTGAGACTT 29

RESULT 39

US-08-353-751-R

Sequence 9, Affiliation: US/08157751

Patent No. 5712113

GENERAL INFORMATION:

```

FILE REFERENCE: 233-134
CURRENT APPLICATION NUMBER: 08-09-197-650-25
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 61763-147
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 50
LENGTH: 25
TYPE: DNA
TRANSLATION: Not defined
08-09-197-650-25

CY      1  GATTGCGCAGACGA 18    41.0%   Score 13.0, DB 4, Length 25,
DB      5  GTTCTGTGGCAGACGA 22    32.0%   E-value 1.0e-03,
Matched 15, Conserved 10, 1 Mismatch, 1 Gap

RESULT 34
CS-09-656-952-5/C
Sequence 5, Affiliation: Not annotated
Patent No. 6444443
GENERAL INFORMATION:
APPLICANT: Gaber, Jai et al.
TITLE OF INVENTION: NO. 6444443-1 Gene
FILE REFERENCE: 314061/N/HO 2
CURRENT APPLICATION NUMBER: US/99/056,952
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
TRANSLATION: Homo sapiens
CS-09-656-952-5

CY      9  GGACAGATGTTTCTCT 29    43.0%   Score 15, DB 4, Length 29,
DB     22  GGACAGATGATGTTTACT 2    36.0%   E-value 1.0e-03,
Matched 16, Conserved 10, 1 Mismatch, 1 Gap

RESULT 35
CS-09-684-340-1163/C
Sequence 1163, Affiliation: Not annotated
Patent No. 6447404
GENERAL INFORMATION:
APPLICANT: Esau, Fred L
APPLICANT: Moschese, James
APPLICANT: Stinnett, David T.
APPLICANT: Esterhuysen, John
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VITAMIN E ENZYME ACTIVITY
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2056
COMPUTER READABLE FORM:

```

```

1 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
2 MEDIUM TYPE: Storage
3 COMPUTER: IBM compatible
4 OPERATING SYSTEM: IBM PC, DOS 5.0
5 SOFTWARE: Word Perfect 5.1
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: 03/08/584,040
8 FILING DATE: January 11, 1996
9 CLASSIFICATION: 514
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 60/060,974
12 FILING DATE: October 10, 1995
13 AUTHOR/INVENTOR INFORMATION:
14 NAME: Warburg, Richard J.
15 REGISTRATION NUMBER: 37,327
16 REFERENCE/SEQUENCE INFORMATION:
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (213) 489-1600
19 TELEFAX: (213) 905-0440
20 TELETYPE: 67-7510
21 INFORMATION FOR SEQ ID NO: 1:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 27 base pairs
24 TYPE: nucleic acid
25 FEATURES:
26 TOPOLOGY: linear
27 OTHER INFORMATION: The letter "N" represents the stem 11 region
28 OTHER INFORMATION: of an mRNA molecule.
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
```

```

RESULT 30
US-09-252-508B-1
Sequence 1, Application US/980255999
Patent No. 5854017
GENERAL INFORMATION:
APPLICANT: Palese, Peter
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7692-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 799-9000
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-252-508B-1

Query Match          44.0%  Score 13.27  DB 6;  Length 21;
Best Local Similarity 83.3%  Field No. 1, 2a+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

CY 12 AAGAGAAATTTTCTCT 29
CG 12 AAGAGAAATTTTCTCT 19
CG 12 AAGAGAAATTTTCTCT 19

RESULT 31
US-09-106-377-1
Sequence 1, Application US/90106177
Patent No. 6001634
GENERAL INFORMATION:
APPLICANT: Palese, Peter
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7692-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 799-9000
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-106-377-1

Query Match          44.0%  Score 13.27  DB 6;  Length 21;
Best Local Similarity 83.3%  Field No. 1, 2a+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

CY 12 AAGAGAAATTTTCTCT 29
CG 12 AAGAGAAATTTTCTCT 19
CG 12 AAGAGAAATTTTCTCT 19

RESULT 32
US-09-106-377-1
Sequence 1, Application US/90106177
Patent No. 6001634
GENERAL INFORMATION:
APPLICANT: Palese, Peter
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7692-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 799-9000
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-106-377-1

Query Match          44.0%  Score 13.27  DB 6;  Length 21;
Best Local Similarity 83.3%  Field No. 1, 2a+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

CY 12 AAGAGAAATTTTCTCT 29
CG 12 AAGAGAAATTTTCTCT 19
CG 12 AAGAGAAATTTTCTCT 19

RESULT 33
US-09-177-650-50
Sequence 50, Application US/99177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepert, Mark F.
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7692-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 799-9090
TELEFAX: (212) 869-9741/8464
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-106-377-1

Query Match          44.0%  Score 13.27  DB 6;  Length 21;
Best Local Similarity 83.3%  Field No. 1, 2a+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

CY 12 AAGAGAAATTTTCTCT 29
CG 12 AAGAGAAATTTTCTCT 19
CG 12 AAGAGAAATTTTCTCT 19

```

```

SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99177650, 177
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/99177650, 177
FILING DATE: 01-03-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7692-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 799-9090
TELEFAX: (212) 869-9741/8464
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-106-377-1

Query Match          44.0%  Score 13.27  DB 6;  Length 21;
Best Local Similarity 83.3%  Field No. 1, 2a+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

CY 12 AAGAGAAATTTTCTCT 29
CG 12 AAGAGAAATTTTCTCT 19
CG 12 AAGAGAAATTTTCTCT 19

RESULT 32
US-09-177-650-50
Sequence 50, Application US/99177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepert, Mark F.
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7692-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 799-9090
TELEFAX: (212) 869-9741/8464
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-106-377-1

Query Match          44.0%  Score 13.27  DB 6;  Length 21;
Best Local Similarity 83.3%  Field No. 1, 2a+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

CY 12 AAGAGAAATTTTCTCT 29
CG 12 AAGAGAAATTTTCTCT 19
CG 12 AAGAGAAATTTTCTCT 19

RESULT 33
US-09-177-650-50
Sequence 50, Application US/99177650
Patent No. 6413719
GENERAL INFORMATION:
APPLICANT: Lepert, Mark F.
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7692-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 799-9090
TELEFAX: (212) 869-9741/8464
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-106-377-1

Query Match          44.0%  Score 13.27  DB 6;  Length 21;
Best Local Similarity 83.3%  Field No. 1, 2a+03;
Matches 15;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

CY 12 AAGAGAAATTTTCTCT 29
CG 12 AAGAGAAATTTTCTCT 19
CG 12 AAGAGAAATTTTCTCT 19

```

CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 Diskette, 1 44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/476,887A
FILING DATE: June 2, 1994
CLASSIFICATION:
PRIORITY APPLICATION DATA: including application
PRIORITY APPLICATION DATA: described below:
APPLICATION NUMBER: none
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 30,742
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELECOMMUNICATION INFORMATION:
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FIT US94-06311A-37
Query Match 44.0% Score 13.27 Length 31
Best Local Similarity 93.3% (Seq No. 166093)
Matches 14, Conservative 0, Mismatches 0, Gaps 0,
CY 15 AGAGAAATGTTCTGT 29
DB 26 AGAGAAATGTTCTGT 12
BEST 29
US-08-323 192D 1
Sequence 1, Application 05/03/031121
Patent No. 5786199
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEM AND VACCINES
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/476,887A
FILING DATE: 14-OCT-1994
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7642 035
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-323 192D-1
Query Match 44.0% Score 13.27 DB 1 Length 31
Best Local Similarity 43.3% (Seq No. 166093)
Matches 15, Conservative 0, Mismatches 3, Gaps 0,
CY 12 AGAGAAATGTTCTGT 29
DB 2 AGAGAAATGTTCTGT 19
BEST 29
US-08-323 192D-1
Sequence 1, Application 05/03/031121
Patent No. 5820871
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEM AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/476,887A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7642 035
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-323 192D-1
Query Match 44.0% Score 13.27 DB 1 Length 31
Best Local Similarity 43.3% (Seq No. 166093)
Matches 15, Conservative 0, Mismatches 3, Gaps 0,
CY 12 AGAGAAATGTTCTGT 29
DB 2 AGAGAAATGTTCTGT 19

MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' fluoro (2'-F) modified
 FEATURE:
 OTHER INFORMATION: N of position 11 is a 3' 3' linked deoxythymidine
 SEQUENCE INFORMATION: 44 78 Score 13.4 DB 4 Length 28
 US-09-224-968-59 Best Local Similarity 73.98, Field No. 1 54-033
 Matches 12: Conservative 9, Mismatches 2, Indels 0, Gaps 0

QY 6 TCAATGAGCAAGATTTG 24
 6 TCGGTAGCAAGATTTG 22
 ||||| ||||| |||||
 23 TCAATGAGCAAGATTTG 24

US-08 859 998-1356/C
 Sequence 1356, Application US/0859998
 Patent No. 5994076
 GENERAL INFORMATION:
 APPLICANT: Chenchik, Alex
 APPLICANT: Jorhadeze, George
 APPLICANT: Birlashvili, Robert
 TITLE OF INVENTION: METHOD OF ATTACHING DIFFERENTIAL
 NUMBER OF SEQUENCES: 1375
 CLASSIFICATION: 435
 ADDRESS: Fish & Richardson, P.C.
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: CA
 COUNTRY: US
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/859,308
 FILING DATE: 21-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Field, Bret E.
 REGISTRATION NUMBER: 37,620
 PREPARED/DEPT NUMBER: 08/08/7-0001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-322-5070
 TELEFAX: 415-854-0875
 INFORMATION FOR SEQ 16 NO. 1356:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 OTHER INFORMATION: oligonucleotide primer
 SEQUENCE DESCRIPTION: SEQ ID NO. 1356:
 US 09 225 928-1356

Query Match 44 78 Score 13.4 DB 4 Length 28
 Best Local Similarity 73.98, Field No. 1 54-033
 Matches 17: Conservative 9, Mismatches 6, Indels 0, Gaps 0

QY 2 TCAATGAGCAAGATTTG 24
 2 TCAATGAGCAAGATTTG 24
 ||||| ||||| |||||
 23 TCAATGAGCAAGATTTG 24

DB 23 TCAATGAGCAAGATTTG 24
 RESULT 26
 US-09-225 928 1356/C
 Sequence 1356, Application US/09-225-928
 Patent No. 6352823
 GENERAL INFORMATION:
 APPLICANT: Chenchik, Alex
 APPLICANT: Jorhadeze, George
 APPLICANT: Birlashvili, Robert
 TITLE OF INVENTION: METHOD OF ATTACHING DIFFERENTIAL
 NUMBER OF SEQUENCES: 1375
 CLASSIFICATION: 435
 ADDRESS: Fish & Richardson, P.C.
 STREET: 2200 Sand Hill Road, Suite 100
 CITY: Menlo Park
 STATE: CA
 COUNTRY: US
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/7-0001
 FILING DATE: 21-May-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Field, Bret E.
 REGISTRATION NUMBER: 37,620
 PREPARED/DEPT NUMBER: 08/08/7-0001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-322-5070
 TELEFAX: 415-854-0875
 INFORMATION FOR SEQ 16 NO. 1356:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 OTHER INFORMATION: oligonucleotide primer
 SEQUENCE DESCRIPTION: SEQ ID NO. 1356:
 US 09 225 928-1356

Query Match 44 78 Score 13.4 DB 4 Length 28
 Best Local Similarity 73.98, Field No. 1 54-033
 Matches 17: Conservative 9, Mismatches 6, Indels 0, Gaps 0

QY 2 TCAATGAGCAAGATTTG 24
 23 TCAATGAGCAAGATTTG 24
 ||||| ||||| |||||
 23 TCAATGAGCAAGATTTG 24

RESULT 27
 PCT US94-06331A-37/C
 Sequence 37, Application PCT/US9406331A
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 TITLE OF INVENTION: METHOD AND REAGENT FOR
 TREATMENT OF PIEROSIS AND
 TITLE OF INVENTION: PIEROSIS TREATMENT
 NUMBER OF SEQUENCES: 67
 CLASSIFICATION: 435
 ADDRESS: Lyon & Lyon
 STREET: 611 West Sixth Street

[illegible]

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/254,968
 FILING DATE: 13-Mar-2000
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US/97/1944
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/733,109
 FILING DATE: 08/07/1997
 APPLICATION NUMBER: 08/733,109
 FILING DATE: 08/07/1997
 APPLICATION NUMBER: 08/733,109
 FILING DATE: 08/07/1997
 APPLICATION NUMBER: 08/733,109
 FILING DATE: 08/07/1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Harry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: NEXT/ECT US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ. 15 NO. 73
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
 modified
 FEATURE:
 OTHER INFORMATION: Indole and 2'-Methyl (2'-OMe) modified
 FEATURE:
 OTHER INFORMATION: G in position 10 and A in position 12 are
 unmodified (1.e., 2'-OH)
 SEQUENCE CHARACTERISTICS: SEQ. 15 NO. 74
 US-09-254-968-73
 Query Match 46.0% Score 13.81 DB 4 Length 29
 Best Local Similarity 70.6% Prod. No. 11e+03
 Matches 12 Conservative 3 Mismatches 21 Indels 02 gaps 02

25 6 TGGGCGAGGAGGANTTG 22
 ||||| |||||
 6 UUUUUUUUUUUUUUUUU 22

RESULT 21
 US-09-254-968-80
 Sequence 80, Application US/09254968
 Patent No. 6426315
 GENERAL INFORMATION:
 APPLICANT: MICHAEL J. JANICE, LARRY G. GIL, PAUL G. SCHWARTZ, MARCIA VANCELE,
 MICHAEL WILLIS
 TITLE OF INVENTION: VACCINE FOR PREVENTING AND TREATING ACID LIQUID COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Katschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/254,968
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US/97/1944
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/733,109
 FILING DATE: 08/07/1997
 APPLICATION NUMBER: 08/733,109
 FILING DATE: 08/07/1997
 APPLICATION NUMBER: 08/733,109
 FILING DATE: 08/07/1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Harry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: NEXT/ECT US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ. 15 NO. 80:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
 modified
 FEATURE:
 OTHER INFORMATION: Furines are 2'-O-methyl (2'-OMe) modified
 FEATURE:
 OTHER INFORMATION: G in positions 10 and 22 are unmodified
 (1.e., 2'-OH)
 SEQUENCE CHARACTERISTICS: SEQ. 15 NO. 81
 US-09-254-968-80
 Query Match 46.0% Score 13.81 DB 4 Length 29
 Best Local Similarity 70.6% Prod. No. 11e+03
 Matches 12 Conservative 3 Mismatches 21 Indels 02 gaps 02

25 6 TGGGCGAGGAGGANTTG 22
 ||||| |||||
 6 UUUUUUUUUUUUUUUUU 22

RESULT 22
 US-09-254-968-81
 Sequence 81, Application US/09254968
 Patent No. 6426315
 GENERAL INFORMATION:
 APPLICANT: MICHAEL J. JANICE, LARRY G. GIL, PAUL G. SCHWARTZ, MARCIA VANCELE,
 MICHAEL WILLIS
 TITLE OF INVENTION: VACCINE FOR PREVENTING AND TREATING ACID LIQUID COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Katschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/254,968
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: Unknown

STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER PEAKABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch, 1.4 Mb storage
COMPILER: IBM compatible
I/O: OPERATING SYSTEM: MVS

SEQUENCE: 111 710
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/254,968
FILING DATE: 18 MAR 2000
CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/US97/18944
FILING DATE: 17 OCTOBER 1997
APPLICATION NUMBER: US/99/109
FILING DATE: 25 OCTOBER 1998
APPLICATION NUMBER: US/99/930
FILING DATE: 6 JUNE 1997
APPLICATION NUMBER: US/97/301
FILING DATE: 21 JULY 1997

ATTORNEY/AGENT INFORMATION:
NAME: BARRY J Swanson
REGISTRATION NUMBER: 23,015
REFERENCE: SOCIETY NUMBER, MEMBERSHIP-UTS
TELEPHONE: 303 733 3333
TELEFAX: (303) 733 3433
E-MAIL: bswanson@att.net

INFORMATION FOR SRS ID NO: 78:
SEQUENCE: 111 710

LENGTH: 29
TYPE: nucleic acid
STRANDEDNESS: single
ISOTOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All primers are 2' flanked by P modified

FEATURE:
OTHER INFORMATION: Enzymes are 2' C-methyl 2' O-m modified

FEATURE:
OTHER INFORMATION: 2' N position 12, A at position 17, and G in position 22 are unmodified (1.e., 2'-OH)

SEQUENCE: 111 710
SEQUENCE: 111 710

Query Match: 4e-04 Score 13.97 LR 47 Depth 237
Best Local Similarity: 100% (Seq No 110-07)
Matches: 10, Conservative: 2, Mismatches: 2, Indels: 0, Gap: 0

RESULT 20
US 99 254 968-79
Patent No. 6428335
GENERAL INFORMATION:
AFFILIANT: HERGENROTTER, LARRY BOED, PAUL D. STENITZ, MARIA WACHNER
MICHAEL WILLIS
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
HOMES OF INVENTORS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8430 East Frontline Avenue, Suite #400
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:

REFERENCE/DOCKET NUMBER: NEX61
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 74
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are
 OTHER INFORMATION: 2'-fluoro (2'-OME) modified
 FEATURE:
 OTHER INFORMATION: Purines are
 OTHER INFORMATION: 2'-O-methyl (2'-OME) modified
 FEATURE:
 OTHER INFORMATION: 3 in position 10, A in position 12,
 OTHER INFORMATION: and G in position 22 are unmodified (1.00, 2'-OH)
 US-09-870-930-76

Query Match 46.0% Score 13.8; DB 4; Length 29;
 Best Local Similarity 70.6% (Fid. No. 116+03)
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

QY 6 TGGGACAGGAGGAGATG 22
 DB 6 TGGGACAGGAGGAGATG 22

US-09-870-930-75

RESULT 16
 US-09-870-930-75
 Reference 75, Application US/9870930
 Patent No. 6168778
 GENERAL INFORMATION:
 APPLICANT: NEROLISA JANITO, LARRY GOLD, PAUL G. SWANSON, CHANILPA VAPASESE, MICHAEL
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
 TITLE OF INVENTION: NUCLEIC ACID LIBRARY COMPLEXES
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Ratschuh, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/870,930
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: NEX61
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 75:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro
 OTHER INFORMATION: unmodified (1.00, 2'-OH)
 US-09-870-930-76

OTHER INFORMATION: 1 in position 10 and A in
 OTHER INFORMATION: 2'-OME modified
 FEATURE:
 OTHER INFORMATION: G in position 10 and A in
 OTHER INFORMATION: position 12 are unmodified (1.00, 2'-OH)
 US-09-870-930-75

Query Match 46.0% Score 13.8; DB 4; Length 29;
 Best Local Similarity 70.6% (Fid. No. 116+03)
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

QY 6 TGGGACAGGAGGAGATG 22
 DB 6 TGGGACAGGAGGAGATG 22

US-09-870-930-76

RESULT 17
 US-09-870-930-76
 Reference 76, Application US/09870930
 Patent No. 6168778
 GENERAL INFORMATION:
 APPLICANT: NEROLISA JANITO, LARRY GOLD, PAUL G. SWANSON, CHANILPA VAPASESE, MICHAEL
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
 TITLE OF INVENTION: NUCLEIC ACID LIBRARY COMPLEXES
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Ratschuh, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/ 97/ 870,930
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: NEX61
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 76:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro
 OTHER INFORMATION: 2'-O-methyl
 OTHER INFORMATION: 2'-OME modified
 FEATURE:
 OTHER INFORMATION: 3 in positions 10 and 22 is
 OTHER INFORMATION: unmodified (1.00, 2'-OH)
 US-09-870-930-76

Query Match 46.0% Score 13.8; DB 4; Length 29;
 Best Local Similarity 70.6% (Fid. No. 116+03)
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

QY 6 TGGGACAGGAGGAGATG 22
 DB 6 TGGGACAGGAGGAGATG 22

STREET: 8400 East Frontage Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 25 OCTOBER 1996
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 6 JUNE 1997
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 21 JULY 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Barry C. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/AGENT NUMBER: 08/08/964,964
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 OTHER INFORMATION: All pyrimidines are 2'-fluoro 2'-F modified

SEQUENCE DESCRIPTION: SEQ ID NO: 60:
 US-09-254-968-60

Query Match: 46.0% Score 13.8; DB 4; Length 28;
 Best Local Similarity 70.6% Pred. No. 1,1e+03;
 Matches 12; Conservative 3; Wt. 1.0; Index 0; Gaps 0;

CY 6 TGGCGAGAGAGATG 22
 DB 6 UGGGAGAGAGAGAG 22

RESULT 14
 US-08-870-930-61

Sequence 71: Amino Acid: 73
 Patent No. 6168778
 GENERAL INFORMATION:
 APPLICANT: MERRICK GANTZ, JEFFREY J. FAY, D. SCHWARTZ, CHANDEA VANDERKAM
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
 NUMBER OF SEQUENCES: 88
 ADDRESS: Swanson and Spatschun, P.L.C.
 STREET: 8400 East Frontage Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry C. Swanson
 REGISTRATION NUMBER: 33,215

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 25 OCTOBER 1996
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 6 JUNE 1997
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 21 JULY 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Barry C. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/AGENT NUMBER: 08/08/964,964
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 OTHER INFORMATION: All pyrimidines are 2'-fluoro 2'-F modified

SEQUENCE DESCRIPTION: SEQ ID NO: 61:
 US-09-254-968-61

Query Match: 46.0% Score 13.8; DB 4; Length 28;
 Best Local Similarity 70.6% Pred. No. 1,1e+03;
 Matches 12; Conservative 3; Wt. 1.0; Index 0; Gaps 0;

CY 6 TGGCGAGAGAGATG 22
 DB 5 UGGGAGAGAGAGAG 21

RESULT 15
 US-08-870-930-74

Sequence 71: Amino Acid: 73
 Patent No. 6168778
 GENERAL INFORMATION:
 APPLICANT: MERRICK GANTZ, JEFFREY J. FAY, D. SCHWARTZ, CHANDEA VANDERKAM
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
 NUMBER OF SEQUENCES: 88
 ADDRESS: Swanson and Spatschun, P.L.C.
 STREET: 8400 East Frontage Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/964,964
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry C. Swanson
 REGISTRATION NUMBER: 33,215

Patent No. 611067
GENERAL INFORMATION:
APPLICANT: E. M. J. HUGGINS
APPLICANT: HUGGINS, LAUREN S.
APPLICANT: LALION, MICHAEL
APPLICANT: KUGERA, PEBBICA B.
APPLICANT: SCHILDKRAUT, IRA
TITLE OF INVENTION: Cloning and Producing The N-Bacchi Nicking Endonuclease
FILE REFERENCE: NEB 178
CURRENT APPLICATION NUMBER: US09/096,715
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ. NO. 27
SOFTWARE: Patent In Ver. 2.0
SEQ. NO. 17
LENGTH: 25
TYPE: DNA
ORGANISM: Bacillus stearothermophilus
US 09-586-935-17

Query Match 46.0%; Score 14; DB 4; Length 25;
Best Local Similarity 77.38; Freq. No. 8,326,02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

6 TGGGAGAGAGAAAGTCTT 2/
24 TGGGAGAGAGAAAGTCTT 3

RESULT 11
US 08-870-930-56

Sequence 56; Application US/08/0428
Patent No. 6168778

GENERAL INFORMATION:
APPLICANT: NEBOGA JANITA, LARRY GOLD, PAUL G. SCHMITT, CHARLPA VARGHESE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:
ADDRESS: Swanson and Bratschun, L.L.C.

STREET: 4400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US08/410,400

FILING DATE: 6 JUNE 1997

CLASSIFICATION: 536

ATTORNEY/AGENT: M. J. VARGHESE

NAME: Entry 1 Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/SEQUENCE NUMBER: NEB1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER: IN SEQUENCE: All pyrimidines are 2' fluorine

Query Match 46.0%; Score 14; DB 4; Length 28;
Best Local Similarity 70.61; Freq. No. 1,126,03;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

6 TGGGAGAGAGAAAGTCTT 22
24 TGGGAGAGAGAAAGTCTT 22

RESULT 12
US-08-870-930-57

Sequence 57; Application US/08/0970930
Patent No. 6168778

GENERAL INFORMATION:
APPLICANT: NEBOGA JANITA, LARRY GOLD, PAUL G. SCHMITT, CHARLPA VARGHESE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:
ADDRESS: Swanson and Bratschun, L.L.C.

STREET: 4400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,930

FILING DATE: 6 JUNE 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Entry 1 Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/SEQUENCE NUMBER: NEB61

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER: INFORMATION: All pyrimidines are 2' fluorine

Query Match 46.0%; Score 13.8; DB 4; Length 28;
Best Local Similarity 70.61; Freq. No. 1,126,03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

6 TGGGAGAGAGAAAGTCTT 22
24 TGGGAGAGAGAAAGTCTT 22

RESULT 13
US-09-254-968-60

Sequence 60; Application US/09/254,968
Patent No. 6426335

GENERAL INFORMATION:
APPLICANT: NEBOGA JANITA, LARRY GOLD, PAUL G. SCHMITT, CHARLPA VARGHESE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:
ADDRESS: Swanson and Bratschun, L.L.C.

STREET: 4400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

1 NAME: CHARLES A. MOSBRITAN
2 REGISTRATION NUMBER: 14,664
3 REFERENCE/ACCOUNT NUMBER: 156,1153
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 212-661-8009
6 TELEFAX: 212-661-8002
7 INFORMATION FOR SEQU ID NO. 100
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 24
10 TYPE: MOLECULE
11 STRAINED/NO. SINGLE
12 TOPOLGY: LINEAR
13 MOLECULE TYPE: OLIGONUCLEOTIDE
14 FEATURE:
15 NAME/REF.
16 OTHER INFORMATION: TYPE " Alpha 1
17 75-08-437-353A.75

Query Match: 46.7% Score 14, PF 5, Length 24,
 Best Local Similarity: 77.3%, Seed No. 6, 20002,
 Matched: 17, Conserved: 5, Mutations: 5, Indels: 0, Gaps:
 0
 7 GGGGAGGAGAGAAATTTTCTG 28
 ||||||| ||||| |||||
 22 GGTGGAGGTGAATTTGCTCTG 1

RESULT 9
 US-08-559-205-467
 Sequence 46, Application US/06553205
 Patent No. 6,274,444
 GENERAL INFORMATION:
 APPLICANT: Dai, Peter C.
 APPLICANT: Dai, Debing
 TITLE OF INVENTION: Methods of identifying plant and animal
 TITLE OF INVENTION: Methods of identifying plant and animal
 NUMBER OF SEQUENCES: 2
 WORKS/SEQUENCES ACCEPTED:
 ADDRESSER: MARSHALL, STEVEN; 3000 N. MARY S DRIVE
 STREET: 6300 South Tower, 7th South Tower Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6403
 COMPUTER FEE/PAID FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/Windows
 SOFTWARE: FASTA; BLAST; BLAST #1.0; Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/091560,206
 FILING DATE:
 CLASSIFICATION: 416
 ATTORNEY/AGENT INFORMATION:
 NAME: Gass, David A.
 REGISTRATION NUMBER: 38,113
 REFERENCE/POWER NUMBER: 282/33072
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/487,7700
 TELEFAX: 312/487,8448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO. 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-559-205-46

Query Match	Length
Best local	100
Matches	17

	7	GAGGACGGGAAATGTTTCTG	28
67			
id	42	GATGAGCGTGAAAATGGTCGTG	1

RESULT 9
US-04-041-0008-4173
Sequence 43; Application US/09041090B
Patent No. 6114516
GENERAL INFORMATION:
INVENTOR: BERMAN, BERNARD; FRIEDBERG, FREDERICK;
ATTORNEY: ELMAN & MANN, SERGIO, ENGLAND, JACQUES
TITLE OF INVENTION: METHOD FOR SEPARATING STAIN FROM TEXTILE
FIELD OF INVENTION: FIELD OF THE ARTS, BRANCH OF CHEMISTRY AND
SUBCLASSIFICATION: CLASSIFICATION OF THE INVENTION
TITLE OF INVENTION: THERAPEUTIC USES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: BERMAN & MOSERLIAN
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
GENERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,090B
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09,349,172
FILING DATE: 19 APR 1995
APPLICATION NUMBER: PCT/95/00111
FILING DATE: 29 FEB 1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MOSERLIAN
REGISTRATION NUMBER: 19,693
REFERENCE/CITATION NUMBER: 146,1159
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 961-8900
TELEFAX: 212 961-8002
INTERNET FAX SEC ID NO: 43
SEQUENCE CHARACTERISTICS:
VERSION: 24
TYPE: NUCLEOTIDE
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: OLIGONUCLEOTIDE
FEATURES:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER IDENTIFICATION: TYPE "A" ALFA 15, TYPE AR21, POSITION
OTHER INFORMATION: 114
US-09-041-0008-43

	6879	Score	11	18	Length	24
Query Match Statistics:	20.3%	Fold	0.0023			
Matches	17	Covered by	0	Motifs	has	51
				Index		0
QY	/	GCGGACGGAGATGTCTTG	28			
b	/	GCGGACGGAGATGTCTTG	1			

[illegible]

APPLICANT: Strader, C.D.
TITLE OF INVENTION: Human Neutrophil-3 Enzyme
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Mervyn K. O'Connor, Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/084457.171
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/570,168
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Thico, J.E.
REGISTRATION NUMBER: P-35,382
REFERENCE/OTHER NUMBER: 1700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3904
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09 482 371-11
Query March 50.0% Score 16, Length 33,
Best Local Similarity 78.3% Pred. No. 3, 1e+02;
Matches 18, Conservative 0, Mismatches 5, Indels 0;
Gaps 0;
CY 3 MATCGCGTACGAGGAAATGCTT 25
1 MATTCGGCGCGGAGGAAATGCT 23
RESULT 4
US-08-423-393 75/0
Patent No. 6700000
GENERAL INFORMATION:
APPLICANT: HERGEND, THIRREY, TRIBBEL, FERRADINI,
APPLICANT: ROMAN-ROMAN, SERGIO, FERRADINI, LAURENT
TITLE OF INVENTION: VARIABLE REGION OF HUMAN T LYMPH T
TITLE OF INVENTION: RECOMBINANT ANTIBODY BINDING TO THE
TITLE OF INVENTION: RECOMBINANT ANTIBODY BINDING TO THE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRMAN & MUSELMAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/546,072

FILING DATE: 14 APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,510
FILING DATE: 23 NOV 1992
APPLICATION NUMBER: 05/153,700.130
FILING DATE: 12 FEB 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR/91/01613
FILING DATE: 12-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR/91/04703
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSELMAN
REGISTRATION NUMBER: 10,083
REFERENCE/OTHER NUMBER: 146,1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: NUCLEOTIDE
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: OLIGONUCLEOTIDE
FEATURE:
NAME/KEY:
OTHER INFORMATION: TYPE V Alpha 18
US-08-423-393 75
Query March 46.7% Score 14, Length 24,
Best Local Similarity 77.3% Pred. No. 8, 2e+02;
Matches 17, Conservative 0, Mismatches 5, Indels 0;
Gaps 0;
CY 7 GCGGACGAGGAGAAATGCTG 28
22 GTTCACGCTGAAATGCTG 1
RESULT 5
US-08-620-467A-42/C
Sequence 42, Application US/08620467A
Patent No. 5790231
GENERAL INFORMATION:
APPLICANT: HERGEND, THIRREY, TRIBBEL,
APPLICANT: FERRERIO, ROMAN ROMAN, SERGIO, FERRADINI,
APPLICANT: LAURENT
TITLE OF INVENTION: VARIABLE REGION OF THE C-CHAIN OF HUMAN T
TITLE OF INVENTION: RECOMBINANT ANTIBODY BINDING TO THE
TITLE OF INVENTION: RECOMBINANT ANTIBODY BINDING TO THE
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRMAN & MUSELMAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/546,072
FILING DATE: 22 MAR 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/546,072

801	10	25	2	34	PT 0001 0001A-3	Sequence 1, Affi	104	24.7	24	00-00-00-000-00	Sequence 1, Affi
802	10	25	3	35	PT 0002 0002A-3	Sequence 2, Affi	104	24.7	24	00-00-00-000-00	Sequence 2, Affi
803	10	25	4	36	PT 0003 0003A-3	Sequence 3, Affi	104	24.7	24	00-00-00-000-00	Sequence 3, Affi
804	10	25	5	37	PT 0004 0004A-3	Sequence 4, Affi	104	24.7	24	00-00-00-000-00	Sequence 4, Affi
805	10	25	6	38	PT 0005 0005A-3	Sequence 5, Affi	104	24.7	24	00-00-00-000-00	Sequence 5, Affi
806	10	25	7	39	PT 0006 0006A-3	Sequence 6, Affi	104	24.7	24	00-00-00-000-00	Sequence 6, Affi
807	10	25	8	40	PT 0007 0007A-3	Sequence 7, Affi	104	24.7	24	00-00-00-000-00	Sequence 7, Affi
808	10	25	9	41	PT 0008 0008A-3	Sequence 8, Affi	104	24.7	24	00-00-00-000-00	Sequence 8, Affi
809	10	25	10	42	PT 0009 0009A-3	Sequence 9, Affi	104	24.7	24	00-00-00-000-00	Sequence 9, Affi
810	10	25	11	43	PT 0010 0010A-3	Sequence 10, Affi	104	24.7	24	00-00-00-000-00	Sequence 10, Affi
811	10	25	12	44	PT 0011 0011A-3	Sequence 11, Affi	104	24.7	24	00-00-00-000-00	Sequence 11, Affi
812	10	25	13	45	PT 0012 0012A-3	Sequence 12, Affi	104	24.7	24	00-00-00-000-00	Sequence 12, Affi
813	10	25	14	46	PT 0013 0013A-3	Sequence 13, Affi	104	24.7	24	00-00-00-000-00	Sequence 13, Affi
814	10	25	15	47	PT 0014 0014A-3	Sequence 14, Affi	104	24.7	24	00-00-00-000-00	Sequence 14, Affi
815	10	25	16	48	PT 0015 0015A-3	Sequence 15, Affi	104	24.7	24	00-00-00-000-00	Sequence 15, Affi
816	10	25	17	49	PT 0016 0016A-3	Sequence 16, Affi	104	24.7	24	00-00-00-000-00	Sequence 16, Affi
817	10	25	18	50	PT 0017 0017A-3	Sequence 17, Affi	104	24.7	24	00-00-00-000-00	Sequence 17, Affi
818	10	25	19	51	PT 0018 0018A-3	Sequence 18, Affi	104	24.7	24	00-00-00-000-00	Sequence 18, Affi
819	10	25	20	52	PT 0019 0019A-3	Sequence 19, Affi	104	24.7	24	00-00-00-000-00	Sequence 19, Affi
820	10	25	21	53	PT 0020 0020A-3	Sequence 20, Affi	104	24.7	24	00-00-00-000-00	Sequence 20, Affi
821	10	25	22	54	PT 0021 0021A-3	Sequence 21, Affi	104	24.7	24	00-00-00-000-00	Sequence 21, Affi
822	10	25	23	55	PT 0022 0022A-3	Sequence 22, Affi	104	24.7	24	00-00-00-000-00	Sequence 22, Affi
823	10	25	24	56	PT 0023 0023A-3	Sequence 23, Affi	104	24.7	24	00-00-00-000-00	Sequence 23, Affi
824	10	25	25	57	PT 0024 0024A-3	Sequence 24, Affi	104	24.7	24	00-00-00-000-00	Sequence 24, Affi
825	10	25	26	58	PT 0025 0025A-3	Sequence 25, Affi	104	24.7	24	00-00-00-000-00	Sequence 25, Affi
826	10	25	27	59	PT 0026 0026A-3	Sequence 26, Affi	104	24.7	24	00-00-00-000-00	Sequence 26, Affi
827	10	25	28	60	PT 0027 0027A-3	Sequence 27, Affi	104	24.7	24	00-00-00-000-00	Sequence 27, Affi
828	10	25	29	61	PT 0028 0028A-3	Sequence 28, Affi	104	24.7	24	00-00-00-000-00	Sequence 28, Affi
829	10	25	30	62	PT 0029 0029A-3	Sequence 29, Affi	104	24.7	24	00-00-00-000-00	Sequence 29, Affi
830	10	25	31	63	PT 0030 0030A-3	Sequence 30, Affi	104	24.7	24	00-00-00-000-00	Sequence 30, Affi
831	10	25	32	64	PT 0031 0031A-3	Sequence 31, Affi	104	24.7	24	00-00-00-000-00	Sequence 31, Affi
832	10	25	33	65	PT 0032 0032A-3	Sequence 32, Affi	104	24.7	24	00-00-00-000-00	Sequence 32, Affi
833	10	2									

[illegible]

[illegible]

101	12.2	40.7	25	4	US-09-890-363-2	Sequence 22, Affl	174	11.6	38.7	20	1	US-09-890-363-2	Sequence 44, Affl
102	12.2	40.7	30	2	US-09-890-363-2	Sequence 16, Affl	175	11.6	38.7	20	2	US-09-890-363-2	Sequence 17, Affl
103	12.2	40.7	35	3	US-09-890-363-2	Sequence 18, Affl	176	11.6	38.7	20	3	US-09-890-363-2	Sequence 18, Affl
104	12.2	40.7	40	4	US-09-890-363-2	Sequence 19, Affl	177	11.6	38.7	20	4	US-09-890-363-2	Sequence 19, Affl
105	12.2	40.7	45	5	US-09-890-363-2	Sequence 20, Affl	178	11.6	38.7	20	5	US-09-890-363-2	Sequence 20, Affl
106	12.2	40.7	50	6	US-09-890-363-2	Sequence 21, Affl	179	11.6	38.7	20	6	US-09-890-363-2	Sequence 21, Affl
107	12.2	40.7	55	7	US-09-890-363-2	Sequence 22, Affl	180	11.6	38.7	20	7	US-09-890-363-2	Sequence 22, Affl
108	12.2	40.7	60	8	US-09-890-363-2	Sequence 23, Affl	181	11.6	38.7	20	8	US-09-890-363-2	Sequence 23, Affl
109	12.2	40.7	65	9	US-09-890-363-2	Sequence 24, Affl	182	11.6	38.7	20	9	US-09-890-363-2	Sequence 24, Affl
110	12.2	40.7	70	10	US-09-890-363-2	Sequence 25, Affl	183	11.6	38.7	20	10	US-09-890-363-2	Sequence 25, Affl
111	12.2	40.7	75	11	US-09-890-363-2	Sequence 26, Affl	184	11.6	38.7	20	11	US-09-890-363-2	Sequence 26, Affl
112	12.2	40.7	80	12	US-09-890-363-2	Sequence 27, Affl	185	11.6	38.7	20	12	US-09-890-363-2	Sequence 27, Affl
113	12.2	40.7	85	13	US-09-890-363-2	Sequence 28, Affl	186	11.6	38.7	20	13	US-09-890-363-2	Sequence 28, Affl
114	12.2	40.7	90	14	US-09-890-363-2	Sequence 29, Affl	187	11.6	38.7	20	14	US-09-890-363-2	Sequence 29, Affl
115	12.2	40.7	95	15	US-09-890-363-2	Sequence 30, Affl	188	11.6	38.7	20	15	US-09-890-363-2	Sequence 30, Affl
116	12.2	40.7	100	16	US-09-890-363-2	Sequence 31, Affl	189	11.6	38.7	20	16	US-09-890-363-2	Sequence 31, Affl
117	12.2	40.7	105	17	US-09-890-363-2	Sequence 32, Affl	190	11.6	38.7	20	17	US-09-890-363-2	Sequence 32, Affl
118	12.2	40.7	110	18	US-09-890-363-2	Sequence 33, Affl	191	11.6	38.7	20	18	US-09-890-363-2	Sequence 33, Affl
119	12.2	40.7	115	19	US-09-890-363-2	Sequence 34, Affl	192	11.6	38.7	20	19	US-09-890-363-2	Sequence 34, Affl
120	12.2	40.7	120	20	US-09-890-363-2	Sequence 35, Affl	193	11.6	38.7	20	20	US-09-890-363-2	Sequence 35, Affl
121	12.2	40.7	125	21	US-09-890-363-2	Sequence 36, Affl	194	11.6	38.7	20	21	US-09-890-363-2	Sequence 36, Affl
122	12.2	40.7	130	22	US-09-890-363-2	Sequence 37, Affl	195	11.6	38.7	20	22	US-09-890-363-2	Sequence 37, Affl
123	12.2	40.7	135	23	US-09-890-363-2	Sequence 38, Affl	196	11.6	38.7	20	23	US-09-890-363-2	Sequence 38, Affl
124	12.2	40.7	140	24	US-09-890-363-2	Sequence 39, Affl	197	11.6	38.7	20	24	US-09-890-363-2	Sequence 39, Affl
125	12.2	40.7	145	25	US-09-890-363-2	Sequence 40, Affl	198	11.6	38.7	20	25	US-09-890-363-2	Sequence 40, Affl
126	12.2	40.7	150	26	US-09-890-363-2	Sequence 41, Affl	199	11.6	38.7	20	26	US-09-890-363-2	Sequence 41, Affl
127	12.2	40.7	155	27	US-09-890-363-2	Sequence 42, Affl	200	11.6	38.7	20	27	US-09-890-363-2	Sequence 42, Affl
128	12.2	40.7	160	28	US-09-890-363-2	Sequence 43, Affl	201	11.6	38.7	20	28	US-09-890-363-2	Sequence 43, Affl
129	12.2	40.7	165	29	US-09-890-363-2	Sequence 44, Affl	202	11.6	38.7	20	29	US-09-890-363-2	Sequence 44, Affl
130	12.2	40.7	170	30	US-09-890-363-2	Sequence 45, Affl	203	11.6	38.7	20	30	US-09-890-363-2	Sequence 45, Affl
131	12.2	40.7	175	31	US-09-890-363-2	Sequence 46, Affl	204	11.6	38.7	20	31	US-09-890-363-2	Sequence 46, Affl
132	12.2	40.7	180	32	US-09-890-363-2	Sequence 47, Affl	205	11.6	38.7	20	32	US-09-890-363-2	Sequence 47, Affl
133	12.2	40.7	185	33	US-09-890-363-2	Sequence 48, Affl	206	11.6	38.7	20	33	US-09-890-363-2	Sequence 48, Affl
134	12.2	40.7	190	34	US-09-890-363-2	Sequence 49, Affl	207	11.6	38.7	20	34	US-09-890-363-2	Sequence 49, Affl
135	12.2	40.7	195	35	US-09-890-363-2	Sequence 50, Affl	208	11.6	38.7	20	35	US-09-890-363-2	Sequence 50, Affl
136	12.2	40.7	200	36	US-09-890-363-2	Sequence 51, Affl	209	11.6	38.7	20	36	US-09-890-363-2	Sequence 51, Affl
137	12.2	40.7	205	37	US-09-890-363-2	Sequence 52, Affl	210	11.6	38.7	20	37	US-09-890-363-2	Sequence 52, Affl
138	12.2	40.7	210	38	US-09-890-363-2	Sequence 53, Affl	211	11.6	38.7	20	38	US-09-890-363-2	Sequence 53, Affl
139	12.2	40.7	215	39	US-09-890-363-2	Sequence 54, Affl	212	11.6	38.7	20	39	US-09-890-363-2	Sequence 54, Affl
140	12.2	40.7	220	40	US-09-890-363-2	Sequence 55, Affl	213	11.6	38.7	20	40	US-09-890-363-2	Sequence 55, Affl
141	12.2	40.7	225	41	US-09-890-363-2	Sequence 56, Affl	214	11.6	38.7	20	41	US-09-890-363-2	Sequence 56, Affl
142	12.2	40.7	230	42	US-09-890-363-2	Sequence 57, Affl	215	11.6	38.7	20	42	US-09-890-363-2	Sequence 57, Affl
143	12.2	40.7	235	43	US-09-890-363-2	Sequence 58, Affl	216	11.6	38.7	20	43	US-09-890-363-2	Sequence 58, Affl
144	12.2	40.7	240	44	US-09-890-363-2	Sequence 59, Affl	217	11.6	38.7	20	44	US-09-890-363-2	Sequence 59, Affl
145	12.2	40.7	245	45	US-09-890-363-2	Sequence 60, Affl	218	11.6	38.7	20	45	US-09-890-363-2	Sequence 60, Affl
146	12.2	40.7	250	46	US-09-890-363-2	Sequence 61, Affl	219	11.6	38.7	20	46	US-09-890-363-2	Sequence 61, Affl
147	12.2	40.7	255	47	US-09-890-363-2	Sequence 62, Affl	220	11.6	38.7	20	47	US-09-890-363-2	Sequence 62, Affl
148	12.2	40.7	260	48	US-09-890-363-2	Sequence 63, Affl	221	11.6	38.7	20	48	US-09-890-363-2	Sequence 63, Affl
149	12.2	40.7	265	49	US-09-890-363-2	Sequence 64, Affl	222	11.6	38.7	20	49	US-09-890-363-2	Sequence 64, Affl
150	12.2	40.7	270	50	US-09-890-363-2	Sequence 65, Affl	223	11.6	38.7	20	50	US-09-890-363-2	Sequence 65, Affl
151	12.2	40.7	275	51	US-09-890-363-2	Sequence 66, Affl	224	11.6	38.7	20	51	US-09-890-363-2	Sequence 66, Affl
152	12.2	40.7	280	52	US-09-890-363-2	Sequence 67, Affl	225	11.6	38.7	20	52	US-09-890-363-2	Sequence 67, Affl
153	12.2	40.7	285	53	US-09-890-363-2	Sequence 68, Affl	226	11.6	38.7	20	53	US-09-890-363-2	Sequence 68, Affl
154	12.2	40.7	290	54	US-09-890-363-2	Sequence 69, Affl	227	11.6	38.7	20	54	US-09-890-363-2	Sequence 69, Affl
155	12.2	40.7	295	55	US-09-890-363-2	Sequence 70, Affl	228	11.6	38.7	20	55	US-09-890-363-2	Sequence 70, Affl
156	12.2	40.7	300	56	US-09-890-363-2	Sequence 71, Affl	229	11.6	38.7	20	56	US-09-890-363-2	Sequence 71, Affl
157	12.2	40.7	305	57	US-09-890-363-2	Sequence 72, Affl	230	11.6	38.7	20	57	US-09-890-363-2	Sequence 72, Affl
158	12.2	40.7	310	58	US-09-890-363-2	Sequence 73, Affl	231	11.6	38.7	20	58	US-09-890-363-2	Sequence 73, Affl
159	12.2	40.7	315	59	US-09-890-363-2	Sequence 74, Affl	232	11.6	38.7	20	59	US-09-890-363-2	Sequence 74, Affl
160	12.2	40.7	320	60	US-09-890-363-2	Sequence 75, Affl	233	11.6	38.7	20	60	US-09-890-363-2	Sequence 75, Affl
161	12.2	40.7	325	61	US-09-890-363-2	Sequence 76, Affl	234	11.6	38.7	20	61	US-09-890-363-2	Sequence 76, Affl
162	12.2	40.7	330	62	US-09-890-363-2	Sequence 77, Affl	235	11.6	38.7	20	62	US-09-890-363-2	Sequence 77, Affl
163	12.2	40.7	335	63	US-09-890-363-2	Sequence 78, Affl	236	11.6	38.7	20	63	US-09-890-363-2	Sequence 78, Affl
164	12.2	40.7	340	64	US-09-890-363-2	Sequence 79, Affl	237	11.6	38.7	20	64	US-09-890-363-2	Sequence 79, Affl
165	12.2	40.7	345	65	US-09-890-363-2	Sequence 80, Affl	238	11.6	38.7	20	65	US-09-890-363-2	Sequence 80, Affl
166	12.2	40.7	350	66	US-09-890-363-2	Sequence 81, Affl	239	11.6	38.7	20	66	US-09-890-363-2	Sequence 81, Affl
167	12.2	40.7	355	67	US-09-890-363-2	Sequence 82, Affl	240	11.6	38.7	20	67	US-09-890-363-2	Sequence 82, Affl
168	12.2	40.7	360	68	US-09-890-363-2	Sequence 83, Affl	241	11.6	38.7	20	68	US-09-890-363-2	Sequence 83, Affl
169	12.2	40.7	365	69	US-09-890-363-2	Sequence 84, Affl	242	11.6	38.7	20	69	US-09-890-363-2	Sequence 84, Affl
170	12.2	40.7	370	70	US-09-890-363-2	Sequence 85, Affl	243	11.6	38.7	20	70	US-09-890-363-2	Sequence 85, Affl
171	12.2	40.7	375	71	US-09-890-363-2	Sequence 86, Affl	244	11.6	38.7	20	71	US-09-890-363-2	Sequence 86, Affl
172	12.2	40.7	380	72	US-09-890-363-2	Sequence 87, Affl	245	11.6	38.7	20	72	US-09-890-363-2	Sequence 87, Affl
173	12.2	40.7	385	73	US-09-890-363-2	Sequence 88, Affl	246	11.6	38.7	20	73	US-09-890-363-2	Sequence 88, Affl

Wed Jul 23 09:24:53 2003

us-09-890-363-2.max.rng

Page 26

1b 3 5 7 TGGAGGAAAGCAATCTTCGT 25

Search completed: July 21, 2003, 14:05:36
Job time : 116.538 secs

Best Local Similarity 70.48; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 AATTGGCAGAGAGGAAATTTCTGT 29
27 AATTGGCAGAGAGGAAATTTCTTTT 1

RESULT 27
AAV67985
1D AAV67985 standard; DNA; 31 BP.
XX
AC AAV67985;
XX
DT 24-DEC-1998 (first entry)
XX
DE Nucleotide fragment containing polymorphic site, WI-13985 (11).
XX
XX es. polymorphic site, polymorphic analysis, diagnosis, screening,
XX analysis, differential diagnosis, CNS disease.
XX
OS Homo sapiens.
XX
PN W09838846-A2.
XX
XX 11-SEP-1998.
XX
PF 06-MAR-1998; 98WD-US04571.
XX
XX 09-MAR-1997; 97US-0813159.
XX
PR 07-MAR-1997; 97US-0813159.
XX
XX (AFVY) AFFYMETRIX INC.
XX
XX Reino A, Choe M, Fan T, Lifshutz R;
XX
XX WI: 1994-11-17.
XX
XX New nucleic acid segments containing polymorphic sites, of
XX conditions and methods of detecting a nucleic acid - for general
XX use in clinical diagnosis and therapy of disease.
XX
XX Claim 1; Page 29; 42PP; English
XX
XX Now nucleic acid segment consisting of 11-19 100 bp segments
XX given in the specification (sequences of a polymorphic site), or the
XX complement of the segment and a method of analyzing a nucleic acid
XX containing the segment, the base pairing of the polymorphic site of the
XX polymorphic fragment sequences are disclosed in the specification. The
XX invention is directed to a nucleic acid analysis by the method described
XX is useful in diagnosis or monitoring of diseases like cancer,
XX inflammation, heart disease, CNS diseases, and susceptibility to
XX infection by microorganisms. In addition, the nucleic acid segments are
XX useful in manufacturing medication in the treatment of prophylaxis of
XX diseases, and also the use of the DNA segments as pharmaceuticals.
XX
XX Sequence 31 BP; 12 A; 3 C; 9 G; 6 T; 1 other;

Query Match 47.38; Score 14.7; DE 17; Length 31;
Best Local Similarity 76.28; Pred. No. 1.1e+04;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AATTGGCAGAGAGGAAATTTCT 23
5 AATTCAGAGAGAGGAAATTTCT 25

RESULT 28
AAZ08448/C
1D AAZ08448 standard; DNA; 22 BP.
XX
XX AAZ08448;
XX

DE 18-OCT-1999 (first entry)
XX
XX Parathyroid hormone receptor reverse transcriptase PPR primer #1.
DE
XX Osteocalcin osteoblast, osteoblast, bone morphogenic protein, BMP,
XX parathyroid hormone receptor, alkaline phosphatase, proliferation,
XX human, osteoblast precursor cell, OPG, bone defect, osseous defect,
XX traumatic bone loss, congenital insufficiency, malformation,
XX osteoporosis, surgical procedure, treatment, evaluation, bone primer, etc.
XX
XX Synthetic.
XX
OS Homo sapiens.
XX
PN W09939724-A1.
XX
XX 12-AUG-1999.
XX
XX 10-FEB-1999; 99WO-US02946.
XX
XX 12-FEB-1998; 98US-0074451.
XX
XX 10-FEB-1999; 99US-0074450.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Frank E, Hollinger JO, Winn SP, Wong SC;
XX
XX WI: 1999-09-12/41.
XX
XX Composition for treating osseous defects and traumatic bone loss,
XX congenital insufficiency and/or malformations
XX
XX Example 2; Page 23; 81PP; English.
XX
XX The present invention describes composition (1) for treating osseous
XX defects comprising a porous matrix and a cell that is committed to an
XX osteogenic lineage. The composition is useful for healing a bone
XX defect, especially those caused by trauma, fracture, or congenital
XX surgical removal of bone and congenital insufficiency. The
XX composition assists in the repair and regeneration of bone. Embodiment
XX precursor cells (OPCs) have bone-making capability of an OPC and are
XX individual, where OPCs are genetically deficient to form bone.
XX impaired OPCs can be administered to express BMP to repair bone
XX defects. The implant is useful for promoting vascular ingrowth and bone
XX formation, especially in treating bone defects of osteoporosis.
XX The composition, formed with high salt and low density, can be
XX genetically introduced into the cavity without disrupting the cells in the
XX surrounding bone. The present sequence represents a reverse
XX transcription PPR primer used to amplify OPC cells for parathyroid
XX hormone receptor expression.
XX
XX Sequence 22 BP; 6 A; 6 C; 5 G; 5 T; 0 other;

Query Match 46.71; Score 14; DE 20; Length 22;
Best Local Similarity 77.33; Pred. No. 1.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 TGGGAGAGAGAGGAAATTTCT 27
12 TGGGAGAGAGAGGAAATTTCT 1

RESULT 29
AAZ56797/C
1D AAZ56797 standard; DNA; 22 BP.
XX
XX AAZ56797;
XX
XX 04-MAR-2000 (first entry)
XX
XX Parathyroid hormone related protein receptor PPR primer 89; ID No. 1316.

Query Match 51.3% Score 15.4; DB 24; Length 15;
 Best Local Similarity 76.0%; Pred. No. 336e03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0;
 GC 5 TGGCGGCGGCGAGGAAATTTTCTT 29
 DB 3 TGGCGGCGGCGAGGAAATTTTCTT 27

RESULT 11
 AAK71510
 AAK71510 standard; DNA; 35 BP.
 AAK71510
 30-CTU-2002 (first entry)
 CNS related 3' sequencing primer:
 Central nervous system, CNS, neuroleptic, mouse, human, psychosis,
 neurodegenerative disorder, psychiatric disorder, Alzheimer's disease,
 Pick's disease, Parkinson's disease, senile dementia, encephalopathy,
 Parkinson's disease, obsessive-compulsive disorder, epilepsy,
 schizophrenia, addiction, multiple sclerosis, depression;
 manic-depressive disorder; primer; ss.
 XX
 CS Synthetic
 XX
 PN W0200226936 A2.
 XX
 PE 04-APR-2002.
 XX
 PF 01-OCT-2001; 2001W0-0530e05.
 XX
 PR 29-SEP-2000; 4000S-44670P.
 XX
 PS 19-JAN-2001; 2001HS-2639e0P.
 XX
 FA (DIGIT) DIGITAL GENE TECHNOLOGIES INC.
 XX
 PI Thomas EA, Sutcliffe JG, Pribyl TM, Hiltbush ES, Harel KM;
 XX
 DE WPI, 2002-189271/41.
 XX
 PT New polynucleotide useful in gene therapy for preventing, treating,
 PT modulating or activating a cell or a cell line, such as a cell line in a
 PT neuro-psychiatric disorder or a schizophrenia, or a bipolar disorder in
 PT a mammal.
 XX
 PS Example 1; page 233, 254pp, English.

CC This invention relates to the CNS sequences of novel isolated
 CC polynucleotide sequences with 5' and 3' ends at other nucleotide
 CC disorders. The sequences of the invention may act as blockers of D
 CC receptors in the central nervous system. The sequences of the invention
 CC of the invention and the polypeptides encoded by them are useful in the
 CC manufacturing of a reagent useful for preventing, treating, modulating
 CC or ameliorating a medical condition or a neuro-psychiatric disorder. An
 CC antibody that binds the 5' end of the invention is useful for
 CC preventing, treating, modulating or activating neurological disorders
 CC such as psychosis or other neuro-psychiatric disorders in a subject. The
 CC sequence are also useful for diagnosing neurological disorders in a
 CC susceptibility to a neuro-psychiatric disorder such as psychosis and other
 CC neuro-psychiatric disorders in a subject by determining the presence or
 CC absence of mutation in the nucleotide sequence of apolipoprotein B or by
 CC determining the alteration in the expression of the expression of
 CC apolipoprotein B. The sequences of the invention are useful in treating
 CC deficiencies or disorders of the central nervous system or peripheral
 CC nervous system by activating or inhibiting the production of,
 CC differentiation or activity of, or expression of, polypeptides, stem cells
 CC or glial cells. The sequences are useful as a marker of the state of a
 CC particular nervous system disorder or for the treatment of a particular
 CC disorder, Pick's disease, Parkinson's disease, senile dementia,
 CC schizophrenia, addiction, multiple sclerosis, depression, epilepsy,
 CC manic-depressive disorder, obsessive-compulsive disorder, epilepsy,

CC encephalopathy, schizophrenia, addiction, multiple sclerosis, depression
 CC and neuro-psychiatric disorders. The present sequence represents an
 CC polynucleotide primer used in the identification of the above disorders
 CC of the invention.
 XX
 S2 Sequence 35 BP; 3 A; 4 G; 9 T; 0 other;
 Query Match 51.3% Score 15.4; DB 24; Length 15;
 Best Local Similarity 76.0%; Pred. No. 336e03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; GC 5
 GC 5 TGGCGGCGGCGAGGAAATTTTCTT 29
 DB 3 TGGCGGCGGCGAGGAAATTTTCTT 27

RESULT 12
 AAD34664
 ID AAD34664 standard; DNA; 35 BP.
 XX
 AC A634664;
 XX
 CT 16-SEP-2002 (first entry)
 XX
 DE PCR primer #5 used for direct sequencing of TOGA generated PCR products.
 XX
 KW Hepatitis B virus, HBV infection, chronic hepatitis, toxicology, virology,
 KW acute hepatitis, therapeutic, gene therapy, vaccine, infectious diseases,
 KW (TOGA) viral gene expression analysis; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN W0200022783 A2.
 XX
 PE 21 MAR 2002.
 XX
 PF 11-SEP-2001; 4001W0 US20123.
 XX
 PS 15-SEP-2000; 2000DS-233176P.
 XX
 FA (DIGIT) DIGITAL GENE TECHNOLOGIES INC.
 XX
 PI Chisari FV, Michel SF, Guidotti LGVM, Mueller R, Hiltbush ES;
 XX
 DE WPI, 2002-339629/37.
 XX
 PT Preventing and treating hepatitis viral infection in a mammal,
 PT comprising administering nucleic acid molecules that up- or
 PT down-regulate in hepatitis B virus infection a polypeptide encoded by
 PT the nucleic acid molecules.
 XX
 PS Example 1; page 25, 26pp, English.

CC The present invention relates to a method for preventing, treating,
 CC modulating or ameliorating a medical condition. The method involves
 CC administering to a mammal a polypeptide or a down-regulated
 CC polypeptide or a polypeptide of a polypeptide encoded by the
 CC nucleic acid molecules of nucleotides that bind to the polypeptide. The
 CC method is useful for preventing, treating, modulating or activating
 CC a medical condition. It is also useful for determining the presence or
 CC absence of a mutation in the nucleic acid sequence of a gene or
 CC alteration in the expression of the polypeptide which is useful for the
 CC diagnosis of hepatitis viral infection. The method is useful for
 CC assessing the stage of hepatitis viral infection (e.g., acute hepatitis
 CC versus chronic hepatitis), assessing the efficacy of a therapy of
 CC therapeutic treatment for hepatitis viral infection and a gene expression
 CC profile is useful for identifying polypeptides and polynucleotides which
 CC are associated with hepatitis viral infection. Sequences of the invention
 CC are used in gene therapy and as vaccines. Nucleic acid sequences are
 CC useful as a diagnostic marker for HBV infection and for treating
 CC hepatitis B virus. The present DNA sequences are useful for which
 CC are used for direct sequencing of viral viral gene expression analysis
 CC generated for products.

PT polymerside to ceramxin protein
 XX
 PS Example 1: Page 17: 64PP: English
 XX
 CC This invention describes a novel formulation (1) for use in therapeutic
 CC and/or cosmetic treatment of a skin condition, and/or an anti-aging
 CC formulation, and/or a ceramxin protein complexed with a carrier or
 CC vehicle. The primary of the invention have been: preventive, vulnerary,
 CC anti-inflammatory and dermatological activity. (1) is useful in a
 CC formulation (1) which is administered to a site on or within a patient
 CC for the site-specific downregulation of ceramxin protein expression. (1)
 CC is therefore specifically useful for reducing neuronal cell death
 CC resulting from neuronal insult to a specific site in the brain, spinal
 CC cord or peripheral nerve of a patient, for promoting wound healing resulting
 CC from trauma, burns or surgery and for reducing inflammation as a result
 CC of a wound or physical trauma of the brain, spinal cord or peripheral
 CC nerve and for dermal skin formation of a grafting (1) directed to
 CC connective tissue. (1) is administered to regulate epithelial basal cell
 CC division and growth or to regulate outer layer keratinization,
 CC respectively, for skin rejuvenation or thickening for cosmetic or
 CC therapeutic purposes (1) downregulates ceramxin expression in a highly
 CC desirable site-specific manner. This sequence represents a ceramxin-43
 CC directed (1) for use in the which is used in the method of the invention.
 XX
 SQ Sequence 40 Ref: 7 A; 5 C; 9 G; 9 T; 0 other;
 Query Match 69.0%, Score 22.4, DB 21, Length 30,
 Pos: 12.0, 22.0, 22.0, 22.0, 22.0, 22.0, 22.0, 22.0,
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 GTATTTGGGAGGAGGATTTCTCTC 30
 DB 1 GATTTATGACAGGAGGAGGATTTCTCTC 30
 RESULT 5
 AAA09807
 ID AAA09807 standard; DNA; 20 BP.
 XX
 AC AAA09807;
 XX
 DT 24-MAR-1999 (first entry)
 XX
 DE Human biallelic polymorphic marker downstream primer #113.
 XX
 KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW polymorphism; polymorphism; polymorphism; polymorphism; polymorphism;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
 KW treatment; marker; primer; ss
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09620165 A2;
 XX
 PD 14 MAY 1998;
 XX
 PF 05-MAY-1998; 97MO D19911;
 XX
 PR 06-NOV-1998; 96DS-0030455.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 FI Hudson T., 1998: Fr., 400p: Fr.
 XX
 DR WPI: 1998-286974/75
 XX
 PT New isolated nucleic acid sequence from the human genome - used for
 PT determining polymorphic forms for use in - 3 polymorphisms, paternity
 PT testing or forensic testing for disease
 XX
 FT 1998-286974/75, 400p: English

CC AAA099417 X19368 are site-specific oligonucleotide primers used in the
 CC isolation of various biallelic polymorphic markers found in the human
 CC genome (represented in AAA099417-X19368). These primers can be used in a
 CC method for determining polymorphic forms in an individual for use in
 CC e.g. forensic, paternity testing or for therapeutic testing for disease
 CC such as hypercholesterolemia, diabetes mellitus, rheumatoid arthritis,
 CC muscular dystrophy, Wilson's disease, primary biliary cirrhosis, familial
 CC hypercholesterolemia, polycystic kidney disease, hemochromatosis,
 CC hypercholesterolemia, von Willebrand's disease, diabetes mellitus, hemochromatosis,
 CC haemophilia, osteogenesis imperfecta, acute intermittent porphyria,
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 CC autoimmune disease, inflammation, cancer, disease of the nervous
 CC system, infection by pathogenic microorganisms, and immunization with
 CC as adjuvant, appearance of a patient, obesity, growth, speed,
 CC endurance, fertility, and susceptibility to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used in the method of the invention for the treatment of
 CC prophylaxis of such diseases.
 XX
 SQ Sequence 23 BP; 4 A; 2 C; 6 G; 7 T; 0 other;
 Query Match 52.7%, Score 15.8, DB 19, Length 20,
 Pos: 12.0, 22.0, 22.0, 22.0, 22.0, 22.0, 22.0, 22.0,
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 5 GGGAGGAGGAGGATTTCTCTC 27
 DB 2 GGGAGGAGGAGGATTTCTCTC 27
 RESULT 6
 AAA99417
 ID AAA99417 standard; DNA; 28 BP.
 XX
 AC AAA99417;
 XX
 DT 24 JAN 2001 (first entry)
 XX
 DE PCR primer SEQ ID 1 used in L-methionine production.
 XX
 KW L-methionine production; Met; Escherichia coli; PCR primer; ss
 XX
 OS Synthetic.
 XX
 PN JP2000139471-A.
 XX
 ID 23-MAY-2000;
 XX
 PF 17-NOV-1998; 96JP-0196717.
 XX
 PR 17-NOV-1998; 96JP-0326717.
 XX
 PA (AJIN) AJINOMOTO KK.
 XX
 DK WPI: 2001-018703/03.
 XX
 PT Fermentation process for preparation of L-methionine (Met); comparison
 PT using a modified Met-producing organism. The modified organism has
 PT Escherichia species
 XX
 PS Example 1: Page 14: 21PP: Japanese.
 XX
 CC The invention relates to a process for preparing L-methionine (Met)
 CC using a modified Met-producing organism. The modified organism has
 CC its Met biosynthetic system repressor deleted, and has enhanced
 CC homoserine transcarbamoylase activity. The organism preferably has an
 CC attenuated intracellular S-adenosyl methionine synthetase (SAM). The
 CC process is used for the preparation of L-methionine. Sequence AAA99417
 CC and AAA99417 encode primers represented in AAA99417 and AAA99417
 CC respectively, which are derived in the Escherichia coli Met biosynthetic
 CC pathway. AAA99417-A99417 (excluding AAA99417) represent primers; all
 CC sequences are used in the method of the invention for the production of
 CC organism of the invention.

10	15.4	51.3	35	24	ABQ73233
11	15.4	51.3	35	24	ABK75110
12	15.4	51.3	35	24	ABD33555
13	15.2	50.7	25	20	AAK022887
14	15.2	50.7	25	21	AAAZ78994
15	15.2	50.7	25	21	AAAG9555
16	15	50.0	24	24	ABQ037585
17	15	50.0	24	24	AAQ949999
18	15	50.0	24	14	AAQ444777
19	14.5	46.7	32	15	AAQ781544
20	14.6	46.7	32	24	AAQ666233
21	14.4	46.0	30	24	AAK666333
22	14.4	46.0	30	24	AAK666333
23	14.2	47.3	20	21	AAZ755446
24	14.2	47.3	20	22	AAK319205
25	14.2	47.3	20	22	AAK733434
26	14.2	47.3	31	19	AAK698888
27	14.2	47.3	31	19	AAK698888
28	14	46.3	22	21	AAK256715
29	14	46.3	21	13	AAK241915
30	14	46.7	25	22	AAK760991
31	14	46.7	25	22	AAK760991
32	13.8	46.0	20	20	AAZ34835
33	13.8	46.0	20	24	AAK119888
34	13.8	46.0	20	24	AAK119888
35	13.8	44.3	23	24	AAK673293
36	13.4	44.3	23	24	AAK673293
37	13.4	44.3	31	16	AAO812748
38	13.4	44.7	31	19	AAK555334
39	13.4	44.7	31	19	AAK555334
40	13.4	44.7	31	19	AAK555334
41	13.4	44.7	35	24	AAK08990
42	13.4	44.7	35	24	AAK08990
43	13.4	44.7	35	24	AAK08990
44	13.4	44.7	35	24	AAK08990
45	13.4	44.7	35	24	AAK08990
46	13.4	44.7	35	24	AAK08990
47	13.4	44.7	35	24	AAK08990
48	13.4	44.7	35	24	AAK08990
49	13.4	44.7	35	24	AAK08990
50	13.4	44.7	35	24	AAK08990
51	13.4	44.7	35	24	AAK08990
52	13.4	44.7	35	24	AAK08990
53	13.4	44.7	35	24	AAK08990
54	13.4	44.7	35	24	AAK08990
55	13.4	44.7	35	24	AAK08990
56	13.4	44.7	35	24	AAK08990
57	13.4	44.7	35	24	AAK08990
58	13.4	44.7	35	24	AAK08990
59	13.4	44.7	35	24	AAK08990
60	13.4	44.7	35	24	AAK08990
61	13.4	44.7	35	24	AAK08990
62	13.4	44.7	35	24	AAK08990
63	13.4	44.7	35	24	AAK08990
64	13.4	44.7	35	24	AAK08990
65	13.4	44.7	35	24	AAK08990
66	13.4	44.7	35	24	AAK08990
67	13.4	44.7	35	24	AAK08990
68	13.4	44.7	35	24	AAK08990
69	13.4	44.7	35	24	AAK08990
70	13.4	44.7	35	24	AAK08990
71	13.4	44.7	35	24	AAK08990
72	13.4	44.7	35	24	AAK08990
73	13.4	44.7	35	24	AAK08990
74	13.4	44.7	35	24	AAK08990
75	13.4	44.7	35	24	AAK08990
76	13.4	44.7	35	24	AAK08990
77	13.4	44.7	35	24	AAK08990
78	13.4	44.7	35	24	AAK08990
79	13.4	44.7	35	24	AAK08990
80	13.4	44.7	35	24	AAK08990
81	13.4	44.7	35	24	AAK08990
82	13.4	44.7	35	24	AAK089

[illegible]



Db 3 GGAATTCAGCTGAGGAAATTTCTC 28

RESULT 40
AX201854/c

LOCUS

36 bp

DNA

linear

FAT 30 AUG-2001

DEFINITION

Sequence 13 from Patent WO0153494.

ACCESSION

AX201854

VERSION

AX201854.1 GI:15391695

KEYWORDS

STRUCT

synthetic construct.

ORGANISM

synthetic construct.

REFERENCE

artificial sequences.

AUTHORS

1 (bases 1 to 30)

TITLE

Butler, A. and Carter, J. N.

Cloning and overexpression of a small, 130-gelatinase from marine

algae

JOURNAL

Patent: WO 0153494-A 13 26-08-2001

FEATURES

The Regents of the University of California (US)

Location/Qualifiers

1..30

Source

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="DNA"

BASE COUNT

8 a

8 c

5 g

9 t

ORIGIN

Query Match

44.0% Score 13.7, E-6, Length 36,

Best Local Similarity

83.3% Pos: 1-2, 36-35;

Match: 15, Conservation: 0, Mismatch: 3, Indel: 0, Gaps: 0;

QY

2 TAAATGCGGAGAGAGAA 19

CH

18 TTATTGCTGAGAGAGAA 1

Search completed: July 21, 2003, 14:34:49
CPU time: 321.497 secs

REFERENCE 1 (bases 1 to 21)
 AUTHORS Palase, P. and Garcia-Sastre, A.
 TITLE Recombinant negative strand RNA viruses
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="unknown"
 BASE COUNT 4 a 4 c 5 g 7 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 2 AGCAGCAATCTCTCT 19
 RESULT 36
 AX316347
 LOCUS AX316347 29 bp DNA linear PAT 23 JUN 2002
 DEFINITION Sequence 118 from Patent WO0214966.
 ACCESSION AX316347
 VERSION AX316347.1 GI:179202093
 KEYWORDS
 SOURCE synthetic construct;
 ORGANISM synthetic construct;
 REFERENCE 1
 AUTHORS Eickholt, J., van Berghel, J., and van Oort, A.
 TITLE Genes involved in the development of the human
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="synthetic construct"
 ORGANISM /db_xref="taxon:32630"
 REFERENCE 1
 AUTHORS University of Utrecht (NL)
 TITLE Location/Qualifiers
 SOURCE 1..25
 BASE COUNT 7 a 7 c 5 g 6 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 21 CTCATCAATCTCTCT 4
 RESULT 37
 AX441163
 LOCUS AX441163 77 bp DNA linear PAT 23 JUN 2002
 DEFINITION Sequence 110 from Patent WO0215593.
 ACCESSION AX441163
 VERSION AX441163.1 GI:179202094
 KEYWORDS
 SOURCE synthetic construct;
 ORGANISM synthetic construct;
 REFERENCE 1
 AUTHORS Eickholt, J., van Berghel, J., and van Oort, A.
 TITLE Genes involved in the development of the human
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="synthetic construct"
 ORGANISM /db_xref="taxon:32630"
 REFERENCE 1
 AUTHORS University of Utrecht (NL)
 TITLE Location/Qualifiers
 SOURCE 1..27
 BASE COUNT 1 a 27
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 1 27
 RESULT 38
 AX316347
 LOCUS AX316347 29 bp DNA linear PAT 23 JUN 2002
 DEFINITION Sequence 35 from Patent WO0190188.
 ACCESSION AX316347
 VERSION AX316347.1 GI:179202092
 KEYWORDS
 SOURCE synthetic construct;
 ORGANISM synthetic construct;
 REFERENCE 1
 AUTHORS Eickholt, J., van Berghel, J., and van Oort, A.
 TITLE Genes involved in the development of the human
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="synthetic construct"
 ORGANISM /db_xref="taxon:32630"
 REFERENCE 1
 AUTHORS University of Utrecht (NL)
 TITLE Location/Qualifiers
 SOURCE 1..29
 BASE COUNT 8 a 5 c 9 g 7 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 3 GATATCAATCTCTCT 28
 RESULT 39
 AX431255
 LOCUS AX431255 29 bp DNA linear PAT 23 JUN 2002
 DEFINITION Sequence 19 from Patent WO0240543.
 ACCESSION AX431255
 VERSION AX431255.1 GI:121556137
 KEYWORDS
 SOURCE synthetic construct;
 ORGANISM synthetic construct;
 REFERENCE 1
 AUTHORS Eickholt, J., van Berghel, J., and van Oort, A.
 TITLE Genes involved in the development of the human
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="synthetic construct"
 ORGANISM /db_xref="taxon:32630"
 REFERENCE 1
 AUTHORS University of Utrecht (NL)
 TITLE Location/Qualifiers
 SOURCE 1..29
 BASE COUNT 8 a 5 c 9 g 7 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 1 29
 RESULT 40
 AX316347
 LOCUS AX316347 29 bp DNA linear PAT 23 JUN 2002
 DEFINITION Sequence 35 from Patent WO0190188.
 ACCESSION AX316347
 VERSION AX316347.1 GI:179202092
 KEYWORDS
 SOURCE synthetic construct;
 ORGANISM synthetic construct;
 REFERENCE 1
 AUTHORS Eickholt, J., van Berghel, J., and van Oort, A.
 TITLE Genes involved in the development of the human
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="synthetic construct"
 ORGANISM /db_xref="taxon:32630"
 REFERENCE 1
 AUTHORS University of Utrecht (NL)
 TITLE Location/Qualifiers
 SOURCE 1..29
 BASE COUNT 8 a 5 c 9 g 7 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 1 29

BASE COUNT 5 a 8 c 4 g 10 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 24 TCCGCAATCTCTCT 7
 RESULT 38
 AX316347
 LOCUS AX316347 29 bp DNA linear PAT 23 JUN 2002
 DEFINITION Sequence 35 from Patent WO0190188.
 ACCESSION AX316347
 VERSION AX316347.1 GI:179202092
 KEYWORDS
 SOURCE synthetic construct;
 ORGANISM synthetic construct;
 REFERENCE 1
 AUTHORS Eickholt, J., van Berghel, J., and van Oort, A.
 TITLE Genes involved in the development of the human
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="synthetic construct"
 ORGANISM /db_xref="taxon:32630"
 REFERENCE 1
 AUTHORS University of Utrecht (NL)
 TITLE Location/Qualifiers
 SOURCE 1..29
 BASE COUNT 8 a 5 c 9 g 7 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 3 GATATCAATCTCTCT 28
 RESULT 39
 AX431255
 LOCUS AX431255 29 bp DNA linear PAT 23 JUN 2002
 DEFINITION Sequence 19 from Patent WO0240543.
 ACCESSION AX431255
 VERSION AX431255.1 GI:121556137
 KEYWORDS
 SOURCE synthetic construct;
 ORGANISM synthetic construct;
 REFERENCE 1
 AUTHORS Eickholt, J., van Berghel, J., and van Oort, A.
 TITLE Genes involved in the development of the human
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="synthetic construct"
 ORGANISM /db_xref="taxon:32630"
 REFERENCE 1
 AUTHORS University of Utrecht (NL)
 TITLE Location/Qualifiers
 SOURCE 1..29
 BASE COUNT 8 a 5 c 9 g 7 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 1 29
 RESULT 40
 AX316347
 LOCUS AX316347 29 bp DNA linear PAT 23 JUN 2002
 DEFINITION Sequence 35 from Patent WO0190188.
 ACCESSION AX316347
 VERSION AX316347.1 GI:179202092
 KEYWORDS
 SOURCE synthetic construct;
 ORGANISM synthetic construct;
 REFERENCE 1
 AUTHORS Eickholt, J., van Berghel, J., and van Oort, A.
 TITLE Genes involved in the development of the human
 JOURNAL J. Virol. 73:1406-1411 (1999)
 FEATURES
 SOURCE /organism="synthetic construct"
 ORGANISM /db_xref="taxon:32630"
 REFERENCE 1
 AUTHORS University of Utrecht (NL)
 TITLE Location/Qualifiers
 SOURCE 1..29
 BASE COUNT 8 a 5 c 9 g 7 t
 ORIGIN
 Query Match 44.0% Score 13.21 DB 6 Length 21;
 Best Local Similarity 83.3% Prod. No. 2.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 C 1
 Db 1 29

[illegible]

Source	1..28	/organism="unknown"	BASE COUNT	9 a	4 c	11 g	4 t
Query Match	46.0%	Score 13.91	DB 61	Length 29			
Best local similarity	98.2%	Prod No 129076					
Matches	15	Conservation	0	Mismatches	0	Indels	0
Matches	15	Conservation	0	Mismatches	0	Indels	0
ORIGIN							
1							
2							
3							
4							
5							
6							
7							
8							
9							
10							
11							
12							
13							
14							
15							
16							
17							
18							
19							
20							
21							
22							
23							
24							
25							
26							
27							
28							
29							
30							
31							
32							
33							
34							
35							
36							
37							
38							
39							
40							
41							
42							
43							
44							
45							
46							
47							
48							
49							
50							
51							
52							
53							
54							
55							
56							
57							
58							
59							
60							
61							
62							
63							
64							
65							
66							
67							
68							
69							
70							

RESULT 28	AR122854	29 bp	DNA		100%	MAY 1971
LOCUS	AR122854					
DEFINITION	Sequence 76 from patent US 6168778.					
ACCESSION	AF122854					
VERSION	AF122854.1	01-14-1990				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1. Hasegawa I (1979)					
AUTHORS	Janjic N., Gold D., Schmidt P. and Varney M.					
TITLE	Vascular endothelial growth factor (VEGF) nucleotide sequence					
JOURNAL	Patient: US 6168778-A 76 02-72N-2001;					
FEATURES	1..29 bp. CDS(1)..29					
SOURCE	1..29					
EAGE COUNT	3 A 4 C 12 G 4 T					
ORIGIN	/organism="unknown"					
Query Match	46.0% SCORE 15.67 DB 61 Length 29					
Best Local Similarity	89.2% Pred No. 1, 2e+05					
Matches	15; Conservative 2; Indels 0; Mismatches 2					
C	CTGGGAGAGGAAATTC 22					
G						
T	CTGGGAGAGGAAATTC 22					
C	CTGGGAGAGGAAATTC 22					
RESULT 29	AR122855	29 bp	DNA		100%	MAY 1971
LOCUS	AR122855					
DEFINITION	Sequence 77 from patent US 6168778.					
ACCESSION	AF122855					
VERSION	AF122855.1	01-14-1990				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1. Hasegawa I (1979)					
AUTHORS	Janjic N., Gold D., Schmidt P. and Varney M.					
TITLE	Vascular endothelial growth factor (VEGF) nucleotide sequence					
JOURNAL	Patient: US 6168778-A 76 02-72N-2001;					
FEATURES	1..29					
SOURCE	1..29					
EAGE COUNT	3 A 4 C 12 G 4 T					
ORIGIN	/organism="unknown"					
Query Match	46.0% SCORE 15.67 DB 61 Length 29					
Best Local Similarity	88.2% Pred No. 1, 2e+05					
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0					
C	CTGGGAGAGGAAATTC 22					
G						
T	CTGGGAGAGGAAATTC 22					
C	CTGGGAGAGGAAATTC 22					
RESULT 30	AR122833	16 bp	DNA		100%	MAY 1971
LOCUS	AR122833					
DEFINITION	Sequence 55 from patent US 6168778.					
ACCESSION	AF122833					
VERSION	AF122833.1	01-14-1979				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1. Hasegawa I (1979)					
AUTHORS	Janjic N., Gold D., Schmidt P. and Varney M.					

Best Loc 17: Conservative 5: Matches 0: Gaps 0:

CY 7 GCGGAGAGAGATGTTTCTG 29
 DB 22 GCGGAGAGATGTTTCTG 1

RESULT 21
 LOCUS 186340/c 21 bp DNA linear EXT 10 MAY 1998

DEFINITION Sequence 75 from Patent US 5700997.
 ACCESSION 186340
 VERSION 186340.1 GI:1426068
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 24)
 Herdant, T., Tihapel, F., Pagan, P., and Pagan, J.
 Nucleotide sequences coding for variable regions of human
 of human T-lymphotropic virus, and specifically peptide segments and
 the diagnostic and therapeutic uses
 Patent: US 5700997-A (5/23/98)

FEATURES
 location/Qualifiers
 1..24

BASE COUNT 6 a 9 c 3 g 6 t
 ORIGIN /organism="Unknown"

Query Match 46.0% Score 14.8 DB 6: Length 24
 Best Local Similarity 72.9% Ext. No. 126405
 Matches 17: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

CY 7 GCGGAGAGAGATGTTTCTG 28
 DB 22 GCGGAGAGATGTTTCTG 1

RESULT 22
 LOCUS AR11122/c 25 bp DNA linear EXT 10 MAY 1998

DEFINITION Sequence 17 from Patent US 5700997.
 ACCESSION AR11122
 VERSION AR11122.1 GI:14119447
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 25)
 Herdant, T., Tihapel, F., Pagan, P., and Pagan, J.
 Nucleotide sequences coding for variable regions of human
 of human T-lymphotropic virus, and specifically peptide segments and
 the diagnostic and therapeutic uses
 Patent: US 5700997-A (5/23/98)

FEATURES
 location/Qualifiers
 1..25

BASE COUNT 7 a 8 c 4 g 6 t
 ORIGIN /organism="Unknown"

Query Match 46.0% Score 14.8 DB 6: Length 25
 Best Local Similarity 72.9% Ext. No. 126405
 Matches 17: Conservative 0: Mismatches 5: Indels 0: Gaps 0:

CY 6 TGGGAGAGAGATGTTTCT 27
 DB 24 TGGGAGAGATGTTTCT 3

RESULT 23
 LOCUS AX02293 23 bp DNA linear EXT 02 NOV 2001
 DEFINITION Sequence 13 from Patent WIPO/01/000000
 ACCESSION AX02293

DEFINITION AX02293.1 GI:14400019
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE
 1
 Zehender, B., Lasser-Pell, U., and Furtner, H.
 Methods and compositions for regulating adipocytes
 Patent: WO 01/42334 A3 (6/11/2001)
 Curtis, Inc. (US)

FEATURES
 location/Qualifiers
 1..23

BASE COUNT 5 a 2 c 10 g 6 t
 ORIGIN /organism="synthetic construct"
 /db_xref="taxon:32610"
 /note="primer"

Query Match 46.0% Score 13.8 DB 6: Length 23
 Best Local Similarity 92.6% Ext. No. 126405
 Matches 15: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

CY 9 GCGGAGAGATGTTTCT 25
 DB 6 GCGGAGAGATGTTTCT 22

RESULT 24
 LOCUS AR122834 28 bp DNA linear EXT 10 MAY 1998

DEFINITION Sequence 56 from Patent US 6106733.
 ACCESSION AR122834
 VERSION AR122834.1 GI:14107600
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 28)
 Janjic, N., Gold, L., Schmidt, P., and Vargese, J.
 Vascular endothelial growth factor (VEGF) Nucleic Acid and
 Complexes
 Patent: US 6106733-A (5/20/2001)

FEATURES
 location/Qualifiers
 1..28

BASE COUNT 9 a 3 c 12 g 4 t
 ORIGIN /organism="Unknown"

Query Match 46.0% Score 13.8 DB 6: Length 28
 Best Local Similarity 92.6% Ext. No. 126405
 Matches 15: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

CY 7 TGGGAGAGAGATGTTTCT 22
 DB 6 TGGGAGAGAGATGTTTCT 22

RESULT 25
 LOCUS AR122835 28 bp DNA linear EXT 10 MAY 1998

DEFINITION Sequence 56 from Patent US 6106733.
 ACCESSION AR122835
 VERSION AR122835.1 GI:14107601
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 1 (bases 1 to 28)
 Janjic, N., Gold, L., Schmidt, P., and Vargese, J.
 Vascular endothelial growth factor (VEGF) Nucleic Acid and
 Complexes
 Patent: US 6106733-A (5/20/2001)

FEATURES
 location/Qualifiers
 1..28

[illegible]

C 942	10.6	35.3	20	6	AX018659	Sequence
C 943	10.6	35.3	20	6	AX018684	Sequence
C 944	10.6	35.3	20	6	AX018681	Sequence
C 945	10.6	35.3	20	6	AX018616	Sequence
C 946	10.6	35.3	20	6	AX019030	Sequence
C 947	10.6	35.3	20	6	AX013480	Sequence
C 948	10.6	35.3	20	6	AX033457	Sequence
C 949	10.6	35.3	20	6	AX149017	Sequence
C 950	10.6	35.3	20	6	AX149047	Sequence
C 951	10.6	35.3	20	6	AX149121	Sequence
C 952	10.6	35.3	20	6	AX233367	Sequence
C 953	10.6	35.3	20	6	AX127342	Sequence
C 954	10.6	35.3	20	6	AX476674	Sequence
C 955	10.6	35.3	20	6	AX033442	Sequence
C 956	10.6	35.3	20	6	B16651	Sequence
C 957	10.6	35.3	20	6	AX029495	Sequence
C 958	10.6	35.3	21	6	AX029495	Sequence
C 959	10.6	35.3	21	6	AX029495	Sequence
C 960	10.6	35.3	21	6	AX097057	Sequence
C 961	10.6	35.3	21	6	AX433933	Sequence
C 962	10.6	35.3	21	6	110043	Sequence
C 963	10.6	35.3	21	6	163359	Sequence
C 964	10.6	35.3	21	12	MMU459759	Mus muscu
C 965	10.6	35.3	21	12	AB069336	Synthetic
C 966	10.6	35.3	22	6	AP030346	Sequence
C 967	10.6	35.3	22	6	AK138774	Sequence
C 968	10.6	35.3	22	6	AK148400	Sequence
C 969	10.6	35.3	22	6	AK148404	Sequence
C 970	10.6	35.3	22	6	AX003313	Sequence
C 971	10.6	35.3	22	12	110044	Sequence
C 972	10.6	35.3	23	6	AP069716	Synthetic
C 973	10.6	35.3	23	6	AP016335	Sequence
C 974	10.6	35.3	23	6	AP023167	Sequence
C 975	10.6	35.3	23	6	AP036809	Sequence
C 976	10.6	35.3	23	6	AP036823	Sequence
C 977	10.6	35.3	23	6	AP157658	Sequence
C 978	10.6	35.3	23	6	AX164289	Sequence
C 979	10.6	35.3	23	6	ES1243	Sequence
C 980	10.6	35.3	23	6	110045	Sequence
C 981	10.6	35.3	23	6	116669	Sequence
C 982	10.6	35.3	23	6	163368	Sequence
C 983	10.6	35.3	24	6	AP159836	Sequence
C 984	10.6	35.3	24	6	AX199424	Sequence
C 985	10.6	35.3	24	6	AX199436	Sequence
C 986	10.6	35.3	24	6	AX030447	Sequence
C 987	10.6	35.3	24	6	110046	Sequence
C 988	10.6	35.3	24	6	110047	Sequence
C 989	10.6	35.3	24	6	110048	Sequence
C 990	10.6	35.3	24	6	110049	Sequence
C 991	10.6	35.3	24	6	AP049707	Sequence
C 992	10.6	35.3	25	6	AP129817	Sequence
C 993	10.6	35.3	25	6	AP161458	Sequence
C 994	10.6	35.3	25	6	AX060764	Sequence
C 995	10.6	35.3	25	6	AX060943	Sequence
C 996	10.6	35.3	25	6	AX117936	Sequence
C 997	10.6	35.3	25	6	AX476652	Sequence
C 998	10.6	35.3	25	6	AX476653	Sequence
C 999	10.6	35.3	25	6	AX476654	Sequence
1000	10.6	35.3	25	6	AX476655	Sequence

ALLEGMENTS

```

REFERENCE
1 (bases 1 to 30)
AUTHORS
Becker, D.L. and Green, C.R.
TITLE
Formulations comprising antisense nucleotides for chemokines
PATENT: WO 0044409-A 2 03 AUG 2000
JOURNAL
RECEIVED: JAVIN, LAWRENCE E. (CFL); JAVIN, LORION (CFL); GREEN, C.R. IN PRIVATE
(NZ)

FEATURES
SOURCE
1
location/Qualifiers
1..30
tag="synthetic construct"
/db_xref="taxon:12630"
/mol_weight="12630"
/mol_weight="12630"

BASE COUNT
6 a 4 c 10 g 10 t

QUERY MATCH
100.0% Score 30.0 DB 6 Length 30
Pos: 100% Identity 100.0% Pos: 30.0 (0.902)
Matches 100% Identical 0 Mismatches 0 Indels 0 Gaps 0

1 GAAATCGAGGAGAGGAAATGTTCTGTC 30
|||||
1 GAAATCGAGGAGAGGAAATGTTCTGTC 30

RESULT 2
AX034829/c
1
AUTHORS
Becker, D.L. and Green, C.R.
TITLE
Formulations comprising antisense nucleotides for chemokines
PATENT: WO 0044409-A 2 03 AUG 2000
JOURNAL
RECEIVED: JAVIN, LAWRENCE E. (CFL); JAVIN, LORION (CFL); GREEN, C.R. IN PRIVATE
(NZ)

FEATURES
SOURCE
1
location/Qualifiers
1..30
tag="synthetic construct"
/db_xref="taxon:12630"
/mol_weight="12630"
/mol_weight="12630"

BASE COUNT
10 a 10 c 4 g 6 t

QUERY MATCH
100.0% Score 30.0 DB 6 Length 30
Pos: 100% Identity 100.0% Pos: 30.0 (0.902)
Matches 100% Identical 0 Mismatches 0 Indels 0 Gaps 0

1 GAAATCGAGGAGAGGAAATGTTCTGTC 30
|||||
1 GAAATCGAGGAGAGGAAATGTTCTGTC 30

```


66	12.8	42.7	23	6	AX123902	AX123902 Sequence	12	42.7	23	6	AX123902	AX123902 Sequence
67	12.8	42.7	23	6	AX123903	AX123903 Sequence	12	42.7	23	6	AX123903	AX123903 Sequence
68	12.8	42.7	23	6	AX123904	AX123904 Sequence	12	42.7	23	6	AX123904	AX123904 Sequence
69	12.8	42.7	23	6	AX123905	AX123905 Sequence	12	42.7	23	6	AX123905	AX123905 Sequence
70	12.8	42.7	23	6	AX123906	AX123906 Sequence	12	42.7	23	6	AX123906	AX123906 Sequence
71	12.8	42.7	23	6	AX123907	AX123907 Sequence	12	42.7	23	6	AX123907	AX123907 Sequence
72	12.8	42.7	23	6	AX123908	AX123908 Sequence	12	42.7	23	6	AX123908	AX123908 Sequence
73	12.8	42.7	23	6	AX123909	AX123909 Sequence	12	42.7	23	6	AX123909	AX123909 Sequence
74	12.8	42.7	23	6	AX123910	AX123910 Sequence	12	42.7	23	6	AX123910	AX123910 Sequence
75	12.8	42.7	23	6	AX123911	AX123911 Sequence	12	42.7	23	6	AX123911	AX123911 Sequence
76	12.8	42.7	23	6	AX123912	AX123912 Sequence	12	42.7	23	6	AX123912	AX123912 Sequence
77	12.8	42.7	23	6	AX123913	AX123913 Sequence	12	42.7	23	6	AX123913	AX123913 Sequence
78	12.8	42.7	23	6	AX123914	AX123914 Sequence	12	42.7	23	6	AX123914	AX123914 Sequence
79	12.8	42.7	23	6	AX123915	AX123915 Sequence	12	42.7	23	6	AX123915	AX123915 Sequence
80	12.8	42.7	23	6	AX123916	AX123916 Sequence	12	42.7	23	6	AX123916	AX123916 Sequence
81	12.8	42.7	23	6	AX123917	AX123917 Sequence	12	42.7	23	6	AX123917	AX123917 Sequence
82	12.8	42.7	23	6	AX123918	AX123918 Sequence	12	42.7	23	6	AX123918	AX123918 Sequence
83	12.8	42.7	23	6	AX123919	AX123919 Sequence	12	42.7	23	6	AX123919	AX123919 Sequence
84	12.8	42.7	23	6	AX123920	AX123920 Sequence	12	42.7	23	6	AX123920	AX123920 Sequence
85	12.8	42.7	23	6	AX123921	AX123921 Sequence	12	42.7	23	6	AX123921	AX123921 Sequence
86	12.8	42.7	23	6	AX123922	AX123922 Sequence	12	42.7	23	6	AX123922	AX123922 Sequence
87	12.8	42.7	23	6	AX123923	AX123923 Sequence	12	42.7	23	6	AX123923	AX123923 Sequence
88	12.8	42.7	23	6	AX123924	AX123924 Sequence	12	42.7	23	6	AX123924	AX123924 Sequence
89	12.8	42.7	23	6	AX123925	AX123925 Sequence	12	42.7	23	6	AX123925	AX123925 Sequence
90	12.8	42.7	23	6	AX123926	AX123926 Sequence	12	42.7	23	6	AX123926	AX123926 Sequence
91	12.8	42.7	23	6	AX123927	AX123927 Sequence	12	42.7	23	6	AX123927	AX123927 Sequence
92	12.8	42.7	23	6	AX123928	AX123928 Sequence	12	42.7	23	6	AX123928	AX123928 Sequence
93	12.8	42.7	23	6	AX123929	AX123929 Sequence	12	42.7	23	6	AX123929	AX123929 Sequence
94	12.8	42.7	23	6	AX123930	AX123930 Sequence	12	42.7	23	6	AX123930	AX123930 Sequence
95	12.8	42.7	23	6	AX123931	AX123931 Sequence	12	42.7	23	6	AX123931	AX123931 Sequence
96	12.8	42.7	23	6	AX123932	AX123932 Sequence	12	42.7	23	6	AX123932	AX123932 Sequence
97	12.8	42.7	23	6	AX123933	AX123933 Sequence	12	42.7	23	6	AX123933	AX123933 Sequence
98	12.8	42.7	23	6	AX123934	AX123934 Sequence	12	42.7	23	6	AX123934	AX123934 Sequence
99	12.8	42.7	23	6	AX123935	AX123935 Sequence	12	42.7	23	6	AX123935	AX123935 Sequence
100	12.8	42.7	23	6	AX123936	AX123936 Sequence	12	42.7	23	6	AX123936	AX123936 Sequence
101	12.8	42.7	23	6	AX123937	AX123937 Sequence	12	42.7	23	6	AX123937	AX123937 Sequence
102	12.8	42.7	23	6	AX123938	AX123938 Sequence	12	42.7	23	6	AX123938	AX123938 Sequence
103	12.8	42.7	23	6	AX123939	AX123939 Sequence	12	42.7	23	6	AX123939	AX123939 Sequence
104	12.8	42.7	23	6	AX123940	AX123940 Sequence	12	42.7	23	6	AX123940	AX123940 Sequence
105	12.8	42.7	23	6	AX123941	AX123941 Sequence	12	42.7	23	6	AX123941	AX123941 Sequence
106	12.8	42.7	23	6	AX123942	AX123942 Sequence	12	42.7	23	6	AX123942	AX123942 Sequence
107	12.8	42.7	23	6	AX123943	AX123943 Sequence	12	42.7	23	6	AX123943	AX123943 Sequence
108	12.8	42.7	23	6	AX123944	AX123944 Sequence	12	42.7	23	6	AX123944	AX123944 Sequence
109	12.8	42.7	23	6	AX123945	AX123945 Sequence	12	42.7	23	6	AX123945	AX123945 Sequence
110	12.8	42.7	23	6	AX123946	AX123946 Sequence	12	42.7	23	6	AX123946	AX123946 Sequence
111	12.8	42.7	23	6	AX123947	AX123947 Sequence	12	42.7	23	6	AX123947	AX123947 Sequence
112	12.8	42.7	23	6	AX123948	AX123948 Sequence	12	42.7	23	6	AX123948	AX123948 Sequence
113	12.8	42.7	23	6	AX123949	AX123949 Sequence	12	42.7	23	6	AX123949	AX123949 Sequence
114	12.8	42.7	23	6	AX123950	AX123950 Sequence	12	42.7	23	6	AX123950	AX123950 Sequence
115	12.8	42.7	23	6	AX123951	AX123951 Sequence	12	42.7	23	6	AX123951	AX123951 Sequence
116	12.8	42.7	23	6	AX123952	AX123952 Sequence	12	42.7	23	6	AX123952	AX123952 Sequence
117	12.8	42.7	23	6	AX123953	AX123953 Sequence	12	42.7	23	6	AX123953	AX123953 Sequence
118	12.8	42.7	23	6	AX123954	AX123954 Sequence	12	42.7	23	6	AX123954	AX123954 Sequence
119	12.8	42.7	23	6	AX123955	AX123955 Sequence	12	42.7	23	6	AX123955	AX123955 Sequence
120	12.8	42.7	23	6	AX123956	AX123956 Sequence	12	42.7	23	6	AX123956	AX123956 Sequence
121	12.8	42.7	23	6	AX123957	AX123957 Sequence	12	42.7	23	6	AX123957	AX123957 Sequence
122	12.8	42.7	23	6	AX123958	AX123958 Sequence	12	42.7	23	6	AX123958	AX123958 Sequence
123	12.8	42.7	23	6	AX123959	AX123959 Sequence	12	42.7	23	6	AX123959	AX123959 Sequence
124	12.8	42.7	23	6	AX123960	AX123960 Sequence	12	42.7	23	6	AX123960	AX123960 Sequence
125	12.8	42.7	23	6	AX123961	AX123961 Sequence	12	42.7	23	6	AX123961	AX123961 Sequence
126	12.8	42.7	23	6	AX123962	AX123962 Sequence	12	42.7	23	6	AX123962	AX123962 Sequence
127	12.8	42.7	23	6	AX123963	AX123963 Sequence	12	42.7	23	6	AX123963	AX123963 Sequence
128	12.8	42.7	23	6	AX123964	AX123964 Sequence	12	42.7	23	6	AX123964	AX123964 Sequence
129	12.8	42.7	23	6	AX123965	AX123965 Sequence	12	42.7	23	6	AX123965	AX123965 Sequence
130	12.8	42.7	23	6	AX123966	AX123966 Sequence	12	42.7	23	6	AX123966	AX123966 Sequence
131	12.8	42.7	23	6	AX123967	AX123967 Sequence	12	42.7	23	6	AX123967	AX123967 Sequence
132	12.8	42.7	23	6	AX123968	AX123968 Sequence	12	42.7	23	6	AX123968	AX123968 Sequence
133	12.8	42.7	23	6	AX123969	AX123969 Sequence	12	42.7	23	6	AX123969	AX123969 Sequence
134	12.8	42.7	23	6	AX123970	AX123970 Sequence	12	42.7	23	6	AX123970	AX123970 Sequence
135	12.8	42.7	23	6	AX123971	AX123971 Sequence	12	42.7	23	6	AX123971	AX123971 Sequence
136	12.8	42.7	23	6	AX123972	AX123972 Sequence	12	42.7	23	6	AX123972	AX123972 Sequence
137	12.8	42.7	23	6	AX123973	AX123973 Sequence	12	42.7	23	6	AX123973	AX123973 Sequence
138	12.8	42.7	23	6	AX123974	AX123974 Sequence	12	42.7	23	6	AX123974	AX123974 Sequence

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Rm 308, 1100 E. Polk Ave. Salt Lake City, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plates: 0406 Row: K Column: 12
 Seq primer: CACACAGCAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 34.
 Location/Qualifiers

FEATURES

SOURCE

1..34
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="MIMU006K12"
 /clone_id="Mouse 10kb plasmid library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
 /note="Vector: pMD19-1; Purified genomic DNA from M.
 musculus C57BL/6J males was obtained from the Jackson
 Laboratory mouse DNA resource
 (<http://www.jax.org/resources/documents/dnares/>) The DNA
 was hydrolytically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD19 (41473114[gb|AF129272.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

11 a 7 c 5 g 11 t

ORIGIN

Query Match 30 34 Score 11.6 PP 17 Length 34
 Best Local Similarity 77.8% Freq. No. 1.2e-06
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 12 AGGAGAAATGTTCTCT 29
 ||||| ||||| |||||
 Db 29 AAGAAATTTGCTACTCT 12

Search completed: July 21, 2003, 15:45:38
 Job time : 402.76 secs

DEFINITION AV625869.1 34 bp cDNA, unpublished cDNA library from *Hydrobia ulvae*
 cDNA clone: c112c02.5', mRNA sequence.
 ACCESSION AV625869
 VERSION AV625869.1 GI:10459981
 KEYWORDS EST
 SOURCE Clona intestinalis
 ORGANISM Clona intestinalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Actinoptera; Euteleostomi;
 Pleurobranchia; Clonidae; Clona.
 1 (bases 1 to 34)
 Satchi, N., Satchi, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2000)
 CONTACT: Nori Satchi
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, 606-8501, Japan
 Tel: 81-75-753-4061
 Fax: 81-75-705-1113
 Email: satchi@zoology.kyoto-u.ac.jp
 Location/Qualifiers
 1..34
 /organism="Clona intestinalis"
 /db_xref="taxon:7919"
 /clone_id="c112c02.5"
 /tissue_type="whole animal"
 /dev_stage="larva"
 /note="unpublished gene expression EST"

BASE COUNT 4 a 3 c 8 g 10 t
 ORIGIN
 Query Match 36.7% Score 11.6; DB:10 Length 34
 Best Local Similarity 65.4%; Freq. No. 1,2e+06;
 Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0

1 ATTTGGTAAATGATTTTCTGT 29
 2 AATTCGACAGAGCGTTTCTTTT 27

RESULT 38
 AV625869
 LOCUS 34 bp cDNA
 DEFINITION AV625869.1 34 bp cDNA, unpublished cDNA library from *Hydrobia ulvae*
 cDNA clone: c112c02.5', mRNA sequence.
 ACCESSION AV625869
 VERSION AV625869.1 GI:10459981
 KEYWORDS EST
 SOURCE Clona intestinalis
 ORGANISM Clona intestinalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Actinoptera; Euteleostomi;
 Pleurobranchia; Clonidae; Clona.
 1 (bases 1 to 34)
 Satchi, N., Satchi, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2000)
 CONTACT: Nori Satchi
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, 606-8501, Japan
 Tel: 81-75-753-4061
 Fax: 81-75-705-1113
 Email: satchi@zoology.kyoto-u.ac.jp
 Location/Qualifiers
 1..34
 /organism="Clona intestinalis"
 /db_xref="taxon:7919"
 /clone_id="c112c02.5"
 /tissue_type="whole animal"
 /dev_stage="larva"
 /note="unpublished gene expression EST"

BASE COUNT 4 a 3 c 8 g 10 t
 ORIGIN
 Query Match 36.7% Score 11.6; DB:10 Length 34
 Best Local Similarity 65.4%; Freq. No. 1,2e+06;
 Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0

1 ATTTGGTAAATGATTTTCTGT 29
 2 AATTCGACAGAGCGTTTCTTTT 27

RESULT 40
 AZ481979
 LOCUS 34 bp cDNA
 DEFINITION AZ481979.1 34 bp cDNA, unpublished cDNA library from *Hydrobia ulvae*
 cDNA clone: c112c02.5', mRNA sequence.
 ACCESSION AZ481979
 VERSION AZ481979.1 GI:10643044
 KEYWORDS EST
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Actinoptera; Euteleostomi; Pleurobranchia; Clonidae; Clona.
 1 (bases 1 to 34)
 Satchi, N., Satchi, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2000)
 CONTACT: Nori Satchi
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, 606-8501, Japan
 Tel: 81-75-753-4061
 Fax: 81-75-705-1113
 Email: satchi@zoology.kyoto-u.ac.jp
 Location/Qualifiers
 1..34
 /organism="Clona intestinalis"
 /db_xref="taxon:7919"
 /clone_id="c112c02.5"
 /tissue_type="whole animal"
 /dev_stage="larva"
 /note="unpublished gene expression EST"

BASE COUNT 4 a 3 c 8 g 10 t
 ORIGIN
 Query Match 36.7% Score 11.6; DB:10 Length 34
 Best Local Similarity 65.4%; Freq. No. 1,2e+06;
 Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0

1 ATTTGGTAAATGATTTTCTGT 29
 2 AATTCGACAGAGCGTTTCTTTT 27

RESULT 39
 AV625869
 LOCUS 34 bp cDNA
 DEFINITION AV625869.1 34 bp cDNA, unpublished cDNA library from *Hydrobia ulvae*
 cDNA clone: c112c02.5', mRNA sequence.
 ACCESSION AV625869
 VERSION AV625869.1 GI:10459981
 KEYWORDS EST
 SOURCE Clona intestinalis
 ORGANISM Clona intestinalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Actinoptera; Euteleostomi;
 Pleurobranchia; Clonidae; Clona.
 1 (bases 1 to 34)
 Satchi, N., Satchi, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2000)
 CONTACT: Nori Satchi
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, 606-8501, Japan
 Tel: 81-75-753-4061
 Fax: 81-75-705-1113
 Email: satchi@zoology.kyoto-u.ac.jp
 Location/Qualifiers
 1..34
 /organism="Clona intestinalis"
 /db_xref="taxon:7919"
 /clone_id="c112c02.5"
 /tissue_type="whole animal"
 /dev_stage="larva"
 /note="unpublished gene expression EST"

BASE COUNT 4 a 3 c 8 g 10 t
 ORIGIN
 Query Match 36.7% Score 11.6; DB:10 Length 34
 Best Local Similarity 65.4%; Freq. No. 1,2e+06;
 Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0

1 ATTTGGTAAATGATTTTCTGT 29
 2 AATTCGACAGAGCGTTTCTTTT 27

RESULT 40
 AZ481979
 LOCUS 34 bp cDNA
 DEFINITION AZ481979.1 34 bp cDNA, unpublished cDNA library from *Hydrobia ulvae*
 cDNA clone: c112c02.5', mRNA sequence.
 ACCESSION AZ481979
 VERSION AZ481979.1 GI:10643044
 KEYWORDS EST
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Actinoptera; Euteleostomi; Pleurobranchia; Clonidae; Clona.
 1 (bases 1 to 34)
 Satchi, N., Satchi, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2000)
 CONTACT: Nori Satchi
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, 606-8501, Japan
 Tel: 81-75-753-4061
 Fax: 81-75-705-1113
 Email: satchi@zoology.kyoto-u.ac.jp
 Location/Qualifiers
 1..34
 /organism="Clona intestinalis"
 /db_xref="taxon:7919"
 /clone_id="c112c02.5"
 /tissue_type="whole animal"
 /dev_stage="larva"
 /note="unpublished gene expression EST"

ACCESSION R0060604
 VERSION R0060604.1 GI:17499379
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM *Xenopus laevis*
 Eukaryote, Metazoa, Chordata, Vertebrata, Embryophyta, Amphibia, Batrachia, Anura, Mesobatrachia, Pipiloidea, Pipilidae, *Xenopodidae*, *Xenopus*.
 REFERENCE 1 (bases 1 to 11)
 AUTHORS Kiyama, A., Terasawa, C., Matsuda, M., Tanaka, S., Ito, T. and Fukaya, Y.
 TITLE Expressed genes in *X. laevis* embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasi Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tsuhinigenes.nig.ac.jp.
 FEATURES
 Source location/Qualifiers
 1..31
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="X1066101"
 /cdate="11 Nov 2001" /analyzed="Xenopus laevis library"
 /issue_type="embryo stage 15"
 /dev_stage="stage 25"
 /note="Vector property, size 1.1kb, 3'UTR, 5'UTR, CDSs were oligo-dt primed and directionally cloned. Sequencing according to NucleoMap and Fader library is substituted and was constructed by N. Gaitanar and A.M. Zorn, (Wellcome/CRC Institute)."
 BASE COUNT
 G 10 C 10 A 10 T 10
 ORIGIN
 Query Match 38.7% Score 11.6, DR 19, Length 31,
 Best Local Similarity 77.4% Pred. No. 1,2e+06;
 Matches 14, Conservative 0, Mismatches 4, Indels 0, Gaps 0,
 QY 12 AATGAAATTTTCTGT 29
 |||||
 29 AAAAAAATTTTTTTT 12
 RESULT 35
 LOCUS R0033982
 DEFINITION laevis cDNA clone X1066101, cDNA sequence
 ACCESSION R0033982
 VERSION R0033982.1 GI:17499379
 KEYWORDS EST.
 SOURCE African clawed frog
 ORGANISM *Xenopus laevis*
 Eukaryote, Metazoa, Chordata, Vertebrata, Embryophyta, Amphibia, Batrachia, Anura, Mesobatrachia, Pipiloidea, Pipilidae, *Xenopodidae*, *Xenopus*.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Kiyama, A., Terasawa, C., Matsuda, M., Tanaka, S., Ito, T. and Fukaya, Y.
 TITLE Expressed genes in *X. laevis* embryo
 JOURNAL Unpublished (2001)
 COMMENT Contact: Tadasi Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tsuhinigenes.nig.ac.jp.
 FEATURES
 Source location/Qualifiers

SOURCE 1..32
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="X1066102"
 /cdate="11 Nov 2001" /analyzed="Xenopus laevis library"
 /issue_type="whole embryo"
 /dev_stage="stage 15"
 /note="Vector property, size 1.1kb, 3'UTR, 5'UTR, CDSs were oligo-dt primed and directionally cloned. Sequencing according to NucleoMap and Fader library is substituted and was constructed by N. Gaitanar and A.M. Zorn, (Wellcome/CRC Institute)."
 BASE COUNT
 G 5 A 3 C 7 G 17 T
 ORIGIN
 Query Match 38.7% Score 11.6, DR 19, Length 32,
 Best Local Similarity 65.4% Pred. No. 1,2e+06;
 Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0,
 QY 4 AATGCGGACAGAGATTTTCTGT 29
 |||||
 4 AATGCGGACAGAGATTTTCTGT 29
 RESULT 36
 LOCUS AV959846
 DEFINITION AV959846.1 GI:19447145
 ACCESSION AV959846
 VERSION AV959846.1 GI:19447145
 KEYWORDS EST.
 SOURCE Clona intestinalis
 ORGANISM *Clona intestinalis*
 Eukaryote, Metazoa, Chordata, Vertebrata, Embryophyta, Phlebobranchia, Clonidae, Clona.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Sayoh, N., Saito, Y., Fukui, Y. and Shin-i, T.
 TITLE Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2001)
 COMMENT Contact: Nori Saitoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-0113
 Email: satchiasai@zool.kyoto-u.ac.jp.
 FEATURES
 Source location/Qualifiers
 1..33
 /organism="Clona intestinalis"
 /db_xref="taxon:8355"
 /clone="clad1006"
 /cdate="11 Nov 2001" /analyzed="Clona intestinalis library"
 /issue_type="whole animal"
 /dev_stage="young adult"
 /note="Vector property, size 1.1kb, 3'UTR, 5'UTR, CDSs were oligo-dt primed and directionally cloned. Sequencing according to NucleoMap and Fader library is substituted and was constructed by N. Saitoh and A.M. Zorn, (Wellcome/CRC Institute)."
 BASE COUNT
 G 4 A 4 C 6 G 19 T
 ORIGIN
 Query Match 38.7% Score 11.6, DR 19, Length 33,
 Best Local Similarity 65.4% Pred. No. 1,2e+06;
 Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0,
 QY 4 AATGCGGACAGAGATTTTCTGT 29
 |||||
 1 AATGCGGACAGAGATTTTCTGT 26
 RESULT 37
 LOCUS AV975869
 DEFINITION AV975869.1 GI:19447146
 ACCESSION AV975869
 VERSION AV975869.1 GI:19447146
 KEYWORDS EST.
 SOURCE Clona intestinalis
 ORGANISM *Clona intestinalis*
 Eukaryote, Metazoa, Chordata, Vertebrata, Embryophyta, Phlebobranchia, Clonidae, Clona.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Sayoh, N., Saito, Y., Fukui, Y. and Shin-i, T.
 TITLE Expressed genes in Clona intestinalis
 JOURNAL Unpublished (2001)
 COMMENT Contact: Nori Saitoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-0113
 Email: satchiasai@zool.kyoto-u.ac.jp.
 FEATURES
 Source location/Qualifiers

insert site 1 apt. Library--prepared by lining up in the laboratory of Gerald M. Rubin (University of California, Berkeley) using S₁ RNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

100

1

1

1

SOURCE house mouse;
ORGANISM Mus musculus
REFERENCE Eickbush, Wataru, Chittila, Chittila, Yatabuchi, Furukawa, Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus 1 (bases 1 to 33)
AUTHORS Dunn, H., Ayayagi, A., Barber, M., Beaumont, T., Duval, R., Hamill, C., Ielam, H., Longaker, S., Mahmood, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, F., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, F.
TITLE Mouse whole genome scaffolding with paired end reads from 10Xb plasmid inserts
JOURNAL Unpublished (1999)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 302, Biological Sciences Research Bldg., 22 S. 1400 E., Salt Lake City, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7197
Email: dunn@genetics.utah.edu
Insert Length: 10000, Std Error: 0.00
Plates: 0069, Rows: 8, Columns: 10
Seq Primer: CACACAGGACCACTATACG
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1..33
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="mouse" /db_xref="taxon:10090"
/dev_stage="adult"
/seq_id="1" /seq_len="33" /seq_type="text"

Query March 41 38 Score 12.4 DB 17 Length 33
Best local similarity 72 34, Pval 5.6e-051
Matches 16, Mismatches 0, Indels 0, Gaps 0

CY 1 GTAATGGGCAAGAAATG 22
11 GAAATGGGCTTATAATG 22

RESULT 10
COORDS 27 bp, mRNA, Unpub. EST 03/09/1999
COORDS 27 bp, mRNA, Unpub. EST 03/09/1999
DEFINITION Human full (c. 27 bp) cDNA, mRNA
REFERENCE Eickbush, Wataru, Chittila, Chittila, Yatabuchi, Furukawa, Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus 1 (bases 1 to 33)
AUTHORS Dunn, H., Ayayagi, A., Barber, M., Beaumont, T., Duval, R., Hamill, C., Ielam, H., Longaker, S., Mahmood, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, F., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, F.
TITLE Mouse whole genome scaffolding with paired end reads from 10Xb plasmid inserts
JOURNAL Unpublished (1999)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 302, Biological Sciences Research Bldg., 22 S. 1400 E., Salt Lake City, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7197
Email: dunn@genetics.utah.edu
Insert Length: 10000, Std Error: 0.00
Plates: 0069, Rows: 8, Columns: 10
Seq Primer: CACACAGGACCACTATACG
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1..33
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="mouse" /db_xref="taxon:10090"
/dev_stage="adult"
/seq_id="1" /seq_len="33" /seq_type="text"

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eickbush, Wataru, Chittila, Chittila, Yatabuchi, Furukawa, Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo 1 (bases 1 to 27)
AUTHORS Dunn, H., Ayayagi, A., Barber, M., Beaumont, T., Duval, R., Hamill, C., Ielam, H., Longaker, S., Mahmood, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, F., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, F.
TITLE Mouse whole genome scaffolding with paired end reads from 10Xb plasmid inserts
JOURNAL Unpublished (1999)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 302, Biological Sciences Research Bldg., 22 S. 1400 E., Salt Lake City, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7197
Email: dunn@genetics.utah.edu
Insert Length: 10000, Std Error: 0.00
Plates: 0069, Rows: 8, Columns: 10
Seq Primer: CACACAGGACCACTATACG
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1..27
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="human adult (K Ouhos)"
/dev_stage="adult"
/seq_id="1" /seq_len="27" /seq_type="text"

Query March 40 38 Score 12.3 DB 14 Length 27
Best local similarity 92 45, Pval 7e-051
Matches 14, Mismatches 0, Indels 0, Gaps 0

CY 13 AAGAAATTTTCTCT 29
21 AAGAAATTTTCTCT 5

RESULT 11
COORDS 33 bp, mRNA, Unpub. EST 03/09/1999
COORDS 33 bp, mRNA, Unpub. EST 03/09/1999
DEFINITION Human full (c. 33 bp) cDNA, mRNA
REFERENCE Eickbush, Wataru, Chittila, Chittila, Yatabuchi, Furukawa, Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo 1 (bases 1 to 33)
AUTHORS Dunn, H., Ayayagi, A., Barber, M., Beaumont, T., Duval, R., Hamill, C., Ielam, H., Longaker, S., Mahmood, M., Meenan, E., Pedersen, T., Seilly, M., Rose, M., Rose, F., Stokes, F., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, F.
TITLE Mouse whole genome scaffolding with paired end reads from 10Xb plasmid inserts
JOURNAL Unpublished (1999)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 302, Biological Sciences Research Bldg., 22 S. 1400 E., Salt Lake City, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7197
Email: dunn@genetics.utah.edu
Insert Length: 10000, Std Error: 0.00
Plates: 0069, Rows: 8, Columns: 10
Seq Primer: CACACAGGACCACTATACG
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1..27
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="human adult (K Ouhos)"
/dev_stage="adult"
/seq_id="1" /seq_len="27" /seq_type="text"

with adaptors corresponding to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query March 42 78 Score 12.9, PP 17, Length 14,
Best Local Similarity 82.58, Pval NO. 3.9e+05,
Matches 14, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY 10 GAGAGAAAGAAATTTCT 24
DB 10 GAGAGAAAGAAATTTCT 4

RESULT 5
AZ481692 42 bp DNA linear GSS 04-05-2000
LOCUS Mammalian Mouse 1st Plasmid Library Mus musculus genomic
DEFINITION clone insert/insertion F, DNA sequence
ACCESSION AZ481692
VERSION AZ481692.1 GI:10642577
KEYWORDS GSS

SOURCE
ORGANISM

house mouse,
Mus musculus,
Eudoromyia, Mammalia, Chordata, Mammalia, Vertebrata, Euteleostomi,
Mammalia, Euteleostomi, Rodentia, Sciuridae, Muridae, Murinae, Mus,
1 (bases 1 to 42)
Barn, P., Acquisti, A., Parker, M., Reisinger, T., Dwyer, B., Hamel, C.,
Islam, H., Lachy, S., Malmgren, M., Mowbray, F., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, P., Timney, A., von Niederhausen, A.,
and Weisbach, R.,
Mammalian Mouse 1st Plasmid Library Mus musculus genomic
Unpublished (2000)

TITLE
JOURNAL
COMMENT

University of Utah
Contact: Robert B. Weiss
University of Utah Genome Center
Rm 100, 1000 E. 1500 East, Salt Lake City, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunham@genetics.utah.edu
Insert length: 4000 bp
Plasmid length: 4000 bp
Seq primer: GATTTAAGACACGCGCAT
Class: plasmid ends
High quality sequence score: 22
Location/Qualifiers
1..32
/organism="Mus musculus"
/strain="G27BL/6J"
/db_xref="taxon:10088"
/clone="MUSC1M0106C07"
/clone_lib="Mouse 10th plasmid library"
/sex="Male"

with adaptors corresponding to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

with adaptors corresponding to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query March 42 78 Score 12.9, PP 17, Length 20,
Best Local Similarity 78.98, Pval NO. 4.0e+03,
Matches 15, Conservative 0, Mismatches 4, Indels 0, Gaps 0

CY 10 GAGAGAAAGAAATTTCT 28
DB 10 GAGAGAAAGAAATTTCT 21

RESULT 6
AL764935 33 bp DNA linear GSS 19-JUN-2001
LOCUS Arabidopsis thaliana 1 DNA flanking sequence 26,1483 nt (1995),
DEFINITION genomic survey sequence,
ACCESSION AL764935
VERSION AL764935.1 GI:2117078
KEYWORDS GSS,
SOURCE thale cress,
ORGANISM Arabidopsis thaliana,
Eukaryota, Viridiplantae, Euphorbia, Euphorbiaceae, Euphorbia,
Spermatophyta, Magnoliophyta, Eudicotyledons, Core eudicotyledons,
Rosidae, eudicotyledons, Brassicales, Arabidopsida,
1
Stitcher, N., Li, Y., Foster, M., Vandenbroucke, J., Dwyer, B., Dwyer, B.,
and Weisbach, R.,
A pipeline for automated high throughput generation of ESTs
cloning sequences from Arabidopsis thaliana T DNA
transformed lines
Unpublished
2
Foster, M., Stichner, N., Li, Y., Foster, M., Dwyer, B., and Weisbach, R.,
A new Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat
for plant) 3
Unpublished
3 (bases 1 to 33)
Stitcher, N., Foster, M., Li, Y. and Weisbach, R.,
Direct Submission
Submitted (1999) 1000 Weisbach, R., Weisbach, R., Dwyer, B.,
Dwyer, B., Dwyer, B., Dwyer, B., Dwyer, B., Dwyer, B., Dwyer, B.,
This sequence is removed from the right border of the T DNA. It
indicates an insertion within the locus defined by GABI-Kat. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on the
availability can be found at:
http://www.mpi-kreis.de/GABI-Kat/
location/Qualifiers
1..33
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GABI-Kat 10001001"
/clone_lib="Arabidopsis thaliana T DNA insertion lines"
/note="GABI-Kat was performed on DNA from Arabidopsis thaliana
plants (GABI-Kat) which were transformed with the T DNA from
vector GABI-Kat. The library was constructed from T DNA
insertions. The DNA fragment resulting from the PCR
were directly sequenced to determine the insertion sequence.
cloning the insertion sequence directly from the T DNA
similarity to the Arabidopsis thaliana genome sequence were
removed. The T DNA insertion sequences were
removed"

BASE COUNT
ORIGIN

Query March 42 78 Score 12.9, PP 17, Length 20,
Best Local Similarity 78.98, Pval NO. 4.0e+03,
Matches 15, Conservative 0, Mismatches 4, Indels 0, Gaps 0

956 R.R. 29.3 41 9 A1184400
 C 957 R.R. 29.3 31 9 A1444503
 958 R.R. 29.3 31 9 A1677744
 C 959 R.R. 29.3 31 9 A1677744
 C 960 R.R. 29.3 31 9 A1677744
 C 961 R.R. 29.3 31 9 A1677744
 C 962 R.R. 29.3 31 9 A1677744
 C 963 R.R. 29.3 31 9 A1677744
 C 964 R.R. 29.3 31 9 A1677744
 C 965 R.R. 29.3 31 9 A1677744
 C 966 R.R. 29.3 31 9 A1677744
 C 967 R.R. 29.3 31 9 A1677744
 C 968 R.R. 29.3 31 9 A1677744
 C 969 R.R. 29.3 31 9 A1677744
 C 970 R.R. 29.3 31 9 A1677744
 C 971 R.R. 29.3 31 9 A1677744
 C 972 R.R. 29.3 31 9 A1677744
 C 973 R.R. 29.3 31 9 A1677744
 C 974 R.R. 29.3 31 9 A1677744
 C 975 R.R. 29.3 31 9 A1677744
 C 976 R.R. 29.3 31 9 A1677744
 C 977 R.R. 29.3 31 9 A1677744
 C 978 R.R. 29.3 31 9 A1677744
 C 979 R.R. 29.3 31 9 A1677744
 C 980 R.R. 29.3 31 9 A1677744
 C 981 R.R. 29.3 31 9 A1677744
 C 982 R.R. 29.3 31 9 A1677744
 C 983 R.R. 29.3 31 9 A1677744
 C 984 R.R. 29.3 31 9 A1677744
 C 985 R.R. 29.3 31 9 A1677744
 C 986 R.R. 29.3 31 9 A1677744
 C 987 R.R. 29.3 31 9 A1677744
 C 988 R.R. 29.3 31 9 A1677744
 C 989 R.R. 29.3 31 9 A1677744
 C 990 R.R. 29.3 31 9 A1677744
 C 991 R.R. 29.3 31 9 A1677744
 C 992 R.R. 29.3 31 9 A1677744
 C 993 R.R. 29.3 31 9 A1677744
 C 994 R.R. 29.3 31 9 A1677744
 C 995 R.R. 29.3 31 9 A1677744
 C 996 R.R. 29.3 31 9 A1677744
 C 997 R.R. 29.3 31 9 A1677744
 C 998 R.R. 29.3 31 9 A1677744
 C 999 R.R. 29.3 31 9 A1677744
 1000 R.R. 29.3 31 9 A1677744

ALIGNMENTS

RESULT 1
 A2473098/C
 10000
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHOR
 TITLE
 JOURNAL
 COMMENT

10000
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHOR
 TITLE
 JOURNAL
 COMMENT

ALIGNMENTS

RESULT 2
 T3379A05P/C
 10000
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHOR
 TITLE
 JOURNAL
 COMMENT

C 373	9.8	32.7	14	17	A7067306	A2766106	IM033624	446	9.6	32.0	33	14	H761339	H761339	33	14	H761339
C 374	9.8	32.7	14	17	BH864764	BH864764	SALK_0368	447	9.6	32.0	33	17	A2759946	A2759946	33	17	A2759946
C 375	9.8	32.7	35	16	AV654545	AV654545	AV654545	448	9.6	32.0	34	17	BH844814	BH844814	34	17	BH844814
C 376	9.8	32.7	35	17	BH791947	BH791947	SALK_0419	449	9.6	32.0	34	17	AA041949	AA041949	34	17	AA041949
C 377	9.8	32.7	35	17	BH853810	BH853810	SALK_0784	450	9.6	32.0	34	17	A1716467	A1716467	34	17	A1716467
C 378	9.8	32.7	35	17	AL768651	AL768651	Ascidops	451	9.6	32.0	34	17	A1566680	A1566680	34	17	A1566680
C 379	9.6	32.7	15	17	TA755347	TA755347	T. Brucei	452	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 380	9.6	32.0	14	17	A2759946	A2759946	IM033624	453	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 381	9.6	32.0	14	17	A2759946	A2759946	IM033624	454	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 382	9.6	32.0	14	17	A2759946	A2759946	IM033624	455	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 383	9.6	32.0	14	17	A2759946	A2759946	IM033624	456	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 384	9.6	32.0	14	17	A2759946	A2759946	IM033624	457	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 385	9.6	32.0	14	17	A2759946	A2759946	IM033624	458	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 386	9.6	32.0	14	17	A2759946	A2759946	IM033624	459	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 387	9.6	32.0	14	17	A2759946	A2759946	IM033624	460	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 388	9.6	32.0	14	17	A2759946	A2759946	IM033624	461	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 389	9.6	32.0	14	17	A2759946	A2759946	IM033624	462	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 390	9.6	32.0	14	17	A2759946	A2759946	IM033624	463	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 391	9.6	32.0	14	17	A2759946	A2759946	IM033624	464	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 392	9.6	32.0	14	17	A2759946	A2759946	IM033624	465	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 393	9.6	32.0	14	17	A2759946	A2759946	IM033624	466	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 394	9.6	32.0	14	17	A2759946	A2759946	IM033624	467	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 395	9.6	32.0	14	17	A2759946	A2759946	IM033624	468	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 396	9.6	32.0	14	17	A2759946	A2759946	IM033624	469	9.6	32.0	34	17	AA056680	AA056680	34	17	AA056680
C 397	9.6	32.															



1 TITLE OF INVENTION: HUMAN GRAFT METALLOID POLYMER
2 FILE REFERENCE: 2006/006,001
3 CURRENT APPLICATION NUMBER: 2006/006,001
4 CURRENT FILING DATE: 2001-03-27
5 PRIOR APPLICATION NUMBER: 08-01747-510
6 PRIOR FILING DATE: 2000-03-27
7 PRIOR APPLICATION NUMBER: 08-01747-510
8 PRIOR FILING DATE: 2000-03-27
9 NUMBER OF SEQ. ID NOS.: 1403
10 SOFTWARE USED: GENES 5.04
11 SEQ. ID NO.: 1004
12 LENGTH: 31
13 TYPE: DNA
14 ORGANISM: HOMO SAPIENS
15 05-08-901-574-1778

```

CURRENT FILING DATE: 1997-12-15
PRIORITY APPLICATION NUMBER: US 60/064,459
PRIORITY FILING DATE: 1997-12-15
PRIORITY APPLICATION NUMBER: US 60/064,459
PRIORITY FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 16
LENGTH: 23
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-211 9230 16

```

```

Query Match 43.3% Score 13 DB 15 Length 25
Best Local Similarity 76.2% Freq No. 2,56+04
Matches 16 Conservative 0 Mismatches 5 Indels 0 Japs 0
DB 22 GATCAGAGATGTTCTGTC 30
1 GATCAGAGATGTTCTGTC 30

```

```

RESULT 34
US-10-098-263B-49911/c
Sequence 4941/c Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10098263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 49911
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B 49911

```

```

Query Match 43.3% Score 13 DB 15 Length 25
Best Local Similarity 76.2% Freq No. 2,56+04
Matches 16 Conservative 0 Mismatches 5 Indels 0 Japs 0
DB 21 TGTGAGAGATGTTCTGTC 1

```

```

RESULT 35
US-10-098-263B-49911/c
Sequence 4941/c Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10098263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 49912
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-49912

```

```

Query Match 43.3% Score 13 DB 15 Length 25
Best Local Similarity 76.2% Freq No. 2,56+04

```

```

Matches 16 Conservative 0 Mismatches 5 Indels 0 Japs 0
DB 6 TGTGAGAGATGTTCTGTC 26
1 TGTGAGAGATGTTCTGTC 26

```

```

RESULT 36
US-10-098-263B-59654
Sequence 59654 Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10098263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 59654
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B 59654

```

```

Query Match 43.3% Score 13 DB 15 Length 25
Best Local Similarity 76.2% Freq No. 2,56+04
Matches 16 Conservative 0 Mismatches 5 Indels 0 Japs 0
DB 2 GATCAGATGTTCTGTC 22

```

```

RESULT 37
US-10-098-263B-64031/c
Sequence 64031/c Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10098263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 64031
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-64031

```

```

Query Match 43.3% Score 13 DB 15 Length 25
Best Local Similarity 76.2% Freq No. 2,56+04
Matches 16 Conservative 0 Mismatches 5 Indels 0 Japs 0
DB 1 GATCAGATGTTCTGTC 21
2 GATCAGATGTTCTGTC 21

```

```

RESULT 38
US-09-801-274-1778
Sequence 1778 Application US/09801274
Patent No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Gargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.

```


Matches 17, Conservative 0, Mismatches 6, Indels 0, Gaps 0,

QY 7 GGGGCAAGAAATGTTCTGT 29

Db 26 GGTCCAGTAAATCTCTACT 4

RESULT 26

US-10-105-910-16

Sequence 16, Application US/10105730

Publication No. US2001004019A1

GENERAL INFORMATION:

APPLICANT: Matsuda, Masatsugu

APPLICANT ADDRESS: 1-1-1, Kashiwa, Tokyo 135-8501, Japan

TITLE OF INVENTION: NEW PEPTIDE-INDUCED PROTEIN (PROTEIN, SE12

FILE REFERENCE: 06501-105051

CURRENT FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-03

PRIOR APPLICATION NUMBER: JP 11-273358

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Easel for Windows Version 4.1

SEQ ID NO 16

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially synthesized primer sequence

US-10-105-930-16

Query Match

Best Local Similarity 44.8% Score 13.4, DR 15, Length 27,

Best Local Similarity 73.9% Freq No 2, Length 27,

Matches 17, Conservative 0, Mismatches 6, Indels 0, Gaps 0,

QY 7 GGGGCAAGAAATGTTCTGT 29

Db 26 GGTCCAGTAAATCTCTACT 4

RESULT 26

US-10-181-107-43

Sequence 43, Application US/10105730

Publication No. US2001004019A1

GENERAL INFORMATION:

APPLICANT: Hong Zhang

APPLICANT ADDRESS: 100 W. Cowart

TITLE OF INVENTION: ANTISPERM MITIGATION OF ZALFA 2 EXTENSION

FILE REFERENCE: RSP-0325

CURRENT FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: PCT/US01/00898

PRIOR FILING DATE: 2001-01-11

FILE REFERENCE: 06/494,419

PRIOR FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 176

SEQ ID NO 43

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially synthesized primer sequence

US-10-181-107-43

Query Match

Best Local Similarity 44.8% Score 13.4, DR 15, Length 27,

Best Local Similarity 73.9% Freq No 2, Length 27,

Matches 17, Conservative 0, Mismatches 6, Indels 0, Gaps 0,

QY 7 GGGGCAAGAAATGTTCTGT 29

Db 26 GGTCCAGTAAATCTCTACT 4

RESULT 26

US-10-098-263B-117416

Sequence 117416, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

APPLICANT ADDRESS: 100 W. Cowart

TITLE OF INVENTION: HUMAN MICRORNA

FILE REFERENCE: 3118.1

CURRENT FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: 00/226,759

PRIOR FILING DATE: 2000-01-16

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 10

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

OTHER INFORMATION: Sequence listing Generator V 1.1

Matches 13, Conservative 0, Mismatches 8, Indels 0, Gaps 0,

QY 13 AGAAAGATGTTCTGT 10

Db 4 AGAAAGATGTTCTGT 21

RESULT 27

US-10-098-263B-117416

Sequence 117416, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

APPLICANT ADDRESS: 100 W. Cowart

TITLE OF INVENTION: HUMAN MICRORNA

FILE REFERENCE: 3118.1

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 00/226,759

PRIOR FILING DATE: 2001-01-16

FILE REFERENCE: 3118.1

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 10

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

OTHER INFORMATION: Sequence listing Generator V 1.1

US-10-098-263B-117416

Query Match

Best Local Similarity 44.8% Score 13.2, DR 15, Length 27,

Best Local Similarity 73.9% Freq No 2, Length 27,

Matches 13, Conservative 0, Mismatches 8, Indels 0, Gaps 0,

QY 13 AGAAAGATGTTCTGT 10

Db 4 AGAAAGATGTTCTGT 21

RESULT 28

US-10-098-263B-119354/6

Sequence 119354, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

APPLICANT ADDRESS: 100 W. Cowart

TITLE OF INVENTION: HUMAN MICRORNA

FILE REFERENCE: 3118.1

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 00/226,759

PRIOR FILING DATE: 2001-01-16

FILE REFERENCE: 3118.1

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 10

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

OTHER INFORMATION: Sequence listing Generator V 1.1

US-10-098-263B-119354

Query Match

Best Local Similarity 44.8% Score 13.2, DR 15, Length 27,

Best Local Similarity 73.9% Freq No 2, Length 27,

Matches 13, Conservative 0, Mismatches 8, Indels 0, Gaps 0,

QY 13 AGAAAGATGTTCTGT 10

Db 4 AGAAAGATGTTCTGT 21

RESULT 29

US-10-098-263B-126600

Sequence 126600, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

APPLICANT ADDRESS: 100 W. Cowart

TITLE OF INVENTION: HUMAN MICRORNA

FILE REFERENCE: 3118.1

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 00/226,759

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 10

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

OTHER INFORMATION: Sequence listing Generator V 1.1

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 41
 LENGTH: 36
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-237-302-43

Query Match 44.7% Score 13.4 DB 12 Length 36
 Best Local Similarity 92.0% Prog. No. 1.7e+04
 Matches 16 Conserved 0 Mismatches 4 Indels 0 Gaps 0

QY 11 CAGAGCATGTTCTCT 30
 DB 31 CAGAGCATGTTCTCT 12

RESULT 22
 US-09-802-1108-125-6

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 41
 LENGTH: 36
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-237-302-43

Query Match 44.7% Score 13.4 DB 12 Length 36
 Best Local Similarity 92.0% Prog. No. 1.7e+04
 Matches 16 Conserved 0 Mismatches 4 Indels 0 Gaps 0

QY 11 CAGAGCATGTTCTCT 30
 DB 31 CAGAGCATGTTCTCT 12

RESULT 22
 US-09-802-1108-125-6

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 41
 LENGTH: 36
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-237-302-43

Query Match 44.7% Score 13.4 DB 12 Length 36
 Best Local Similarity 92.0% Prog. No. 1.7e+04
 Matches 16 Conserved 0 Mismatches 4 Indels 0 Gaps 0

QY 11 CAGAGCATGTTCTCT 30
 DB 31 CAGAGCATGTTCTCT 12

RESULT 22
 US-09-802-1108-125-6

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 41
 LENGTH: 36
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-237-302-43

Query Match 44.7% Score 13.4 DB 12 Length 36
 Best Local Similarity 92.0% Prog. No. 1.7e+04
 Matches 16 Conserved 0 Mismatches 4 Indels 0 Gaps 0

QY 11 CAGAGCATGTTCTCT 30
 DB 31 CAGAGCATGTTCTCT 12

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 11
 LENGTH: 27
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-105-930-11

Query Match 44.7% Score 13.4 DB 15 Length 27
 Best Local Similarity 92.0% Prog. No. 1.7e+04
 Matches 14 Conserved 0 Mismatches 1 Indels 0 Gaps 0

QY 13 AGAGCATGTTCT 27
 DB 24 AGAGCATGTTCT 10

RESULT 23
 US-10-098-2538-60078-6

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 11
 LENGTH: 27
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-105-930-11

Query Match 44.7% Score 13.4 DB 15 Length 27
 Best Local Similarity 92.0% Prog. No. 1.7e+04
 Matches 14 Conserved 0 Mismatches 1 Indels 0 Gaps 0

QY 13 AGAGCATGTTCT 27
 DB 24 AGAGCATGTTCT 10

RESULT 23
 US-10-098-2538-60078-6

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 11
 LENGTH: 27
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-105-930-11

Query Match 44.7% Score 13.4 DB 15 Length 27
 Best Local Similarity 92.0% Prog. No. 1.7e+04
 Matches 14 Conserved 0 Mismatches 1 Indels 0 Gaps 0

QY 13 AGAGCATGTTCT 27
 DB 24 AGAGCATGTTCT 10

RESULT 23
 US-10-098-2538-60078-6

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 11
 LENGTH: 27
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-105-930-11

Query Match 44.7% Score 13.4 DB 15 Length 27
 Best Local Similarity 92.0% Prog. No. 1.7e+04
 Matches 14 Conserved 0 Mismatches 1 Indels 0 Gaps 0

QY 13 AGAGCATGTTCT 27
 DB 24 AGAGCATGTTCT 10

RESULT 23
 US-10-098-2538-60078-6

APPLICANT: 1st J. Caley
 TITLE OF INVENTION: Aminoacyl tRNA Synthetase
 FILE REFERENCE: 0111-000002
 CURRENT AFFILIATION NUMBER: 02/000000
 CURRENT FILING DATE: 2002-09-06
 PRIOR AFFILIATION NUMBER: 00/000000
 PRIOR FILING DATE: 2001-09-06
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO 11
 LENGTH: 27
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: Description of Artificial Sequence; NOTE =
 OTHER INFORMATION: Synthetic Construct
 US-10-105-930-11

INFORMATION FOR SEQ ID NO: 80:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE: MOLECULE TYPE: RNA
 OTHER INFORMATION: All pyrimidines are 2' fluoro (2' F)
 FEATURE: OTHER INFORMATION: modified
 FEATURE: OTHER INFORMATION: modified
 OTHER INFORMATION: Features are 2' Cw (19) (2' Cw) modified
 FEATURE: OTHER INFORMATION: A in position 10 and 22 is unmodified
 OTHER INFORMATION: unmodified (1.e., 2'-OH)
 US-10-205-009-80
 Query Match: 46.0%, Score 13.0, DP 15, Length 29,
 Best Local Similarity 70.6%, Freq. No. 1.2e+04,
 Mismatch 12, Complement 2, Mismatch 2, Indels 0, Gaps 1
 C 6 TTTGGGAGAGAGATG 22
 |||||
 G UGCGGAGAGAGAUUG 22
 Dt 6 UGCGGAGAGAGAUUG 22
 RESULT 15
 US-10-205-009-81
 Sequence 81, Application US/10205009
 Publication No. US20030114404A1
 GENERAL INFORMATION:
 APPLICANT: REBECCA JANET, LARRY ELLI, ERIC J. SWANSON, SWANSON
 APPLICANT: VAKRSESE,
 TITLE OF INVENTION: VACCINE ENCODING SEQUENCES FOR A PROTEIN
 TITLE OF INVENTION: ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10205009
 FILING DATE: 25-JULY-2002
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10205009
 FILING DATE: 13-Mar-2000
 APPLICATION NUMBER: US/10205009
 FILING DATE: 13-OCTOBER-1997
 APPLICATION NUMBER: US/10205009
 FILING DATE: 25-OCTOBER-1996
 APPLICATION NUMBER: US/10205009
 FILING DATE: 6-JUNE-1997
 APPLICATION NUMBER: 09/897,351
 FILING DATE: 21-JULY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,315
 REFERENCE TO OTHER INFORMATION:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 81:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30
 TYPE: nucleic acid

LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE: OTHER INFORMATION: All pyrimidines are 2' fluoro (2' F)
 FEATURE: OTHER INFORMATION: modified
 FEATURE: OTHER INFORMATION: modified
 OTHER INFORMATION: Features are 2' Cw (19) (2' Cw) modified
 FEATURE: OTHER INFORMATION: A in position 10 and G in position 10 are
 OTHER INFORMATION: unmodified (1.e., 2'-OH)
 US-10-205-009-81
 Query Match: 46.0%, Score 13.0, DP 15, Length 29,
 Best Local Similarity 70.6%, Freq. No. 1.2e+04,
 Mismatch 12, Complement 2, Mismatch 2, Indels 0, Gaps 1
 C 6 TTTGGGAGAGATG 22
 |||||
 G UGCGGAGAGAGAUUG 22
 Dt 6 UGCGGAGAGAGAUUG 22
 RESULT 16
 US-10-205-009-59
 Sequence 59, Application US/10205009
 Publication No. US20030114404A1
 GENERAL INFORMATION:
 APPLICANT: REBECCA JANET, LARRY ELLI, ERIC J. SWANSON, SWANSON
 APPLICANT: VAKRSESE,
 TITLE OF INVENTION: VACCINE ENCODING SEQUENCES FOR A PROTEIN
 TITLE OF INVENTION: ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10205009
 FILING DATE: 25-JULY-2002
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10205009
 FILING DATE: 13-Mar-2000
 APPLICATION NUMBER: US/10205009
 FILING DATE: 13-OCTOBER-1997
 APPLICATION NUMBER: US/10205009
 FILING DATE: 25-OCTOBER-1996
 APPLICATION NUMBER: US/10205009
 FILING DATE: 6-JUNE-1997
 APPLICATION NUMBER: 09/897,351
 FILING DATE: 21-JULY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,315
 REFERENCE TO OTHER INFORMATION:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3433
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30
 TYPE: nucleic acid

REFERENCE/DOCKET NUMBER: NEX01C/PCT US
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 29
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
OTHER INFORMATION: modified
FEATURE:
OTHER INFORMATION: Positions are 2' (modified) 3' (modified)
FEATURE:
OTHER INFORMATION: 4 in position 19, A in position 19, and 4 in
OTHER INFORMATION: position 22 are unmodified (1.e., 2'-OH)
US-10-206-009-24

Query March 40-48: Score 13.4; DB 15; Length 29.
Best Local Similarity 70.6%; Prod. No. 1.2e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0.

09 6 TGGGAGAGAGAGATG 22
DB 6 TGGGAGAGAGAGATG 22

RESULT 13
US-10-206-009-22
Sequence 79, Appl. No. 09/020509
Publication No. US2003014434A1
GENERAL INFORMATION:
APPLICANT: NEBOJSA JANDIC, LARRY GORD, PATT G SCHMITT, CHANPRA
APPLICANT: VARGESE,
APPLICANT: MICHAEL WILLIS
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NOVELTY
TITLE OF INVENTION: ACID LIQUANT COMPLEXES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson and Bratschun, L.L.C.
STREET: 8400 East Flatiron Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/205,009
FILING DATE: 25 JULY 2002
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/054,465
FILING DATE: 13 Mar 2000
APPLICATION NUMBER: PCT/US97/14444
FILING DATE: 17 OCTOBER 1997
APPLICATION NUMBER: 08/733,103
FILING DATE: 25 OCTOBER 1996
APPLICATION NUMBER: 08/470,330
FILING DATE: 6 JUNE 1997
APPLICATION NUMBER: 08/497,351
FILING DATE: 21 JULY 1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01C/PCT US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 29
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
OTHER INFORMATION: modified
FEATURE:
OTHER INFORMATION: Positions are 2' (modified) 3' (modified)
FEATURE:
OTHER INFORMATION: 3 in position 19 and 4 in position 12 are
OTHER INFORMATION: unmodified (1.e., 2'-OH)
US-10-206-009-29

Query March 40-48: Score 13.4; DB 15; Length 29.
Best Local Similarity 70.6%; Prod. No. 1.2e+04;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0.

09 6 TGGGAGAGAGATG 22
DB 6 TGGGAGAGAGATG 22

RESULT 14
US-10-206-009-80
Sequence 80, Application US/1020509
Publication No. US2003014434A1
GENERAL INFORMATION:
APPLICANT: NEBOJSA JANDIC, LARRY GORD, PATT G SCHMITT, CHANPRA
APPLICANT: VARGESE,
APPLICANT: MICHAEL WILLIS
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NOVELTY
TITLE OF INVENTION: ACID LIQUANT COMPLEXES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson and Bratschun, L.L.C.
STREET: 8400 East Flatiron Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/205,009
FILING DATE: 25 JULY 2002
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/054,468
FILING DATE: 13 Mar 2000
APPLICATION NUMBER: PCT/US97/16944
FILING DATE: 17 OCTOBER 1997
APPLICATION NUMBER: 08/733,103
FILING DATE: 25 OCTOBER 1996
APPLICATION NUMBER: 08/470,330
FILING DATE: 6 JUNE 1997
APPLICATION NUMBER: 08/497,351
FILING DATE: 21 JULY 1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01C/PCT US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333

Query Match 46.7% Score 14 DB 15 Length 33
 Best Local Similarity 100.0% Prod No 9 76+03
 Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 6 TGGGCAACAGAA 19
 |||||
 DB 33 TGGGCAACAGAA 20

RESULT 7

US-10-116-248-18/0
 Sequence 18 Application US/1016298
 Publication No. US20020143142A1

GENERAL INFORMATION:
 APPLICANT: Lin, Yao Zhong
 APPLICANT: Donahue, John P.
 APPLICANT: Rojas, Mauricio
 APPLICANT: Tan, Yi Jili

TITLE OF INVENTION: "Sequence and method for genetic engineering of
 TITLE OF INVENTION: Fusion with Cell Membrane Translocating Activity"

FILE REFERENCE: 22000.009703
 CURRENT APPLICATION NUMBER: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-04
 PRIOR FILING DATE: 2002-04-04

Seq ID No 49091
 LENGTH 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-10-099-263P-40091

Query Match 46.0% Score 13.8 DB 15 Length 25
 Best Local Similarity 72.0% Prod No 1 12+04
 Matches 18, Conservative 0, Mismatches 7, Indels 0, Gaps 0

QY 4 ATTGGGCAACAGAAATGGTTG 28
 |||||
 DB 1 AATGGGCAACAGAAATGGTTG 25

RESULT 9

US-10-099-263P-71858/0
 Sequence 60 Application US/10205009
 Publication No. US20030114404A1

GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 APPLICANT: Miltman, Michael

TITLE OF INVENTION: HIV-1 Virus Entry
 TITLE OF INVENTION: HIV-1 Virus Entry

FILE REFERENCE: 2118.1
 CURRENT APPLICATION NUMBER: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

Query Match 46.0% Score 13.8 DB 15 Length 25
 Best Local Similarity 88.2% Prod No 1 12+04
 Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0

QY 13 AAGGCAATGTTACTG 23
 |||||
 DB 23 AAGGCAATGTTACTG 7

RESULT 10

US-10-205-009-60
 Sequence 60 Application US/10205009
 Publication No. US20030114404A1

GENERAL INFORMATION:
 APPLICANT: NEBOJSA JANDIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA
 APPLICANT: NEBOJSA JANDIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA

TITLE OF INVENTION: HIV-1 Virus Entry
 TITLE OF INVENTION: HIV-1 Virus Entry

FILE REFERENCE: 2118.1
 CURRENT APPLICATION NUMBER: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

PRIOR FILING DATE: 2003-01-08
 PRIOR FILING DATE: 2003-01-08

QY 16 A0AMTCTTCTCT 22
 DB 7 A0AMTCTTCTCT 20

RESULT 4

US-10-116-288-16/c

Sequence 16, Application US/01116288
 Publication No. US20020143142A1

GENERAL INFORMATION

APPLICANT: Lin, Yoo Zhong

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of Proteins with Cell Membrane Translocating Activity"

FILE REFERENCE: 2000-009703

CURRENT APPLICATION NUMBER: US/0116-288

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: 02/040,853

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 06/186,170

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 02/018,183

PRIOR FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 16

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence of the protein which translocates

OTHER INFORMATION: Proteins through the cell membrane into the cell

PUBLICATION INFORMATION

AUTHORS: Rojas, M. et al.

TITLE: "Genetic Engineering of Proteins with Cell Membrane

TITLE: Permeability"

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-376

DATE: 1998-04-01

US-10-116-288-16

Query Match: 46.78, Score 14, 26.15, Long 1.77

Best Local Similarity: 100.00, Freq No. 9, 56+03,

Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, gaps: 0

QY 6 TGGCGCAAGAAAGAA 19

DB 24 TGGCGCAAGAAAGAA 11

RESULT 5

US-10-116-288-17/c

Sequence 17, Application US/01116288
 Publication No. US20020143142A1

GENERAL INFORMATION

APPLICANT: Lin, Yoo Zhong

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of Proteins with Cell Membrane Translocating Activity"

FILE REFERENCE: 2000-009703

CURRENT APPLICATION NUMBER: US/0116-288

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: 02/040,853

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 06/186,170

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 06/080,083

PRIOR FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 17

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding peptide which translocates

OTHER INFORMATION: Proteins through the cell membrane into the cell

PUBLICATION INFORMATION

AUTHORS: Rojas, M. et al.

TITLE: "Genetic Engineering of Proteins with Cell Membrane

TITLE: Permeability"

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-376

DATE: 1998-04-01

US-10-116-288-17

Query Match: 46.78, Score 14, 26.15, Long 1.77

Best Local Similarity: 100.00, Freq No. 9, 56+03,

Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, gaps: 0

QY 6 TGGCGCAAGAAAGAA 19

DB 27 TGGCGCAAGAAAGAA 14

RESULT 6

US-10-116-288-17/c

Sequence 17, Application US/01116288
 Publication No. US20020143142A1

GENERAL INFORMATION

APPLICANT: Lin, Yoo Zhong

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of Proteins with Cell Membrane Translocating Activity"

FILE REFERENCE: 2000-009703

CURRENT APPLICATION NUMBER: US/0116-288

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: 02/040,853

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 06/080,083

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 02/018,183

PRIOR FILING DATE: 1998-03-31

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 14

LENGTH: 33

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding peptide which translocates

OTHER INFORMATION: Proteins through the cell membrane into the cell

PUBLICATION INFORMATION

AUTHORS: Rojas, M. et al.

TITLE: "Genetic Engineering of Proteins with Cell Membrane

TITLE: Permeability"

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-376

DATE: 1998-04-01

US-10-116-288-14

[illegible]



DB 1 TGCTACATCGAGATTCTTGCACT 24

RESULT 43

PCT-US95-07744A-19

Sequence 19, Application PCT/US9507744A

GENERAL INFORMATION:

APPLICANT: Trustees of The University of Pennsylvania

TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene

TITLE OF INVENTION: and Pathogens

NUMBER OF SEQUENCE: 92

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, MacArthur, Yurtz, MacKewen & Norris

STREET: One Liberty Place, 16th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIA TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07744A

FILING DATE: 15-JUNE-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/251,822

FILING DATE: June 17, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Beardell, Lori Y.

REGISTRATION NUMBER: 34,293

TELEPHONE: (215) 568-4100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ. ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYDROLYZABLE: NO

ANTI-SENSE: YES

PCT-US95-07744A-19

Query Match

Best Local Similarity 70 at; Pval N=3.5e+03;

Matches 17; Conservation 0; Mismatches 7; Indels 0; Gaps 0;

Query Match

Best Local Similarity 70 at; Pval N=3.5e+03;

Matches 17; Conservation 0; Mismatches 7; Indels 0; Gaps 0;

Query Match

Best Local Similarity 70 at; Pval N=3.5e+03;

Matches 17; Conservation 0; Mismatches 7; Indels 0; Gaps 0;

Query Match

Best Local Similarity 70 at; Pval N=3.5e+03;

Matches 17; Conservation 0; Mismatches 7; Indels 0; Gaps 0;

Query Match

Best Local Similarity 70 at; Pval N=3.5e+03;

Matches 17; Conservation 0; Mismatches 7; Indels 0; Gaps 0;

Query Match

Best Local Similarity 70 at; Pval N=3.5e+03;

Matches 17; Conservation 0; Mismatches 7; Indels 0; Gaps 0;

Query Match

Best Local Similarity 70 at; Pval N=3.5e+03;

Matches 17; Conservation 0; Mismatches 7; Indels 0; Gaps 0;

Search completed: July 21, 2003, 15:48:47

Job time: 37.394 secs

NAME: Batty, J. Swanson
 REGISTRATION NUMBER: 13,215
 REFERENCE/DOCKET NUMBER: NEXUS/ECT 10
 TELECOMMUNICATION INFORMATION
 TELEPHONE: (301) 793-3333
 TELEFAX: (301) 793-3433
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE: OTHER INFORMATION: All pyrimidines are 2' fluorinated.
 FEATURE: modified
 OTHER INFORMATION: C in position 11 is 2' OH C
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-254-968-62

Query Match 42.7% Score 12.4, E 4, Length 23,
 Best Local Similarity 75.0%, Pctd No. 3.5e+03,
 Matches 12, Conservative 2, Mismatches 2, Indels 0, Gaps 0

US-09-254-968-88

US-09-254-968-88
 Patent No. 5650563
 GENERAL INFORMATION:
 APPLICANT: MICROSCA JANET, LARRY GALT, AND R. STEWART, CHAMBERLAIN VANCE, MICHAEL WILLIAMS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NOVELLEID
 NUMBER OF SEQUENCES: 139
 CORRESPONDENT ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: CO 80246
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 M, sec139
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/070,744,000
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/070,744,000
 FILING DATE: 17 October 1997
 APPLICATION NUMBER: 08/730,109
 FILING DATE: 25 October 1996
 APPLICATION NUMBER: 08/870,910
 FILING DATE: 6 June 1997
 APPLICATION NUMBER: 08/897,351
 FILING DATE: 21 July 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Batty, J. Swanson
 REGISTRATION NUMBER: 13,215
 REFERENCE/DOCKET NUMBER: NEXUS/ECT 10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 793-3333
 TELEFAX: (301) 793-3433
 INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE: OTHER INFORMATION: All pyrimidines are 2' fluorinated.
 FEATURE: modified
 OTHER INFORMATION: Purines are 2' modified
 FEATURE: OTHER INFORMATION: Purines are 2' modified
 FEATURE: unmodified (1e, 2'-OH)
 SEQUENCE DESCRIPTION: SEQ ID NO: 88:
 US-09-254-968-88

Query Match 42.7% Score 12.4, E 4, Length 23,
 Best Local Similarity 75.0%, Pctd No. 3.5e+03,
 Matches 12, Conservative 2, Mismatches 2, Indels 0, Gaps 0

US-09-254-968-88

US-09-254-968-88
 Patent No. 5650563
 GENERAL INFORMATION:
 APPLICANT: Baker, Joseph R. et al.
 TITLE OF INVENTION: First In Vivo Test for Detecting the Activity of
 NUMBER OF SEQUENCES: 82
 CORRESPONDENT ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kutz, MacLennan & N. Associates
 STREET: one liberty place, 46th floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/070,744,000
 FILING DATE: 17 JUN-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Beardsell, Lori Y.
 REGISTRATION NUMBER: 34,071
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: YES
 US-09-254-968-19

Query Match 42.7% Score 12.4, E 4, Length 24,
 Best Local Similarity 75.0%, Pctd No. 3.5e+03,
 Matches 17, Conservative 2, Mismatches 7, Indels 0, Gaps 0

US-09-254-968-19

AFFILIATION NUMBER: 7375, 870, 930
 FILING DATE: 6 JUNE 1997
 LOCATION: 139
 ATTORNEY/AGENT INFORMATION:
 NAME: BARRY C. CAMERON
 REGISTRATION NUMBER: 23,215
 REFERENCE/REFEREE NUMBER: 1501
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are
 OTHER INFORMATION: 2'-fluoro (2'-deoxy) modified
 FEATURE:
 OTHER INFORMATION: Edited at 5' end by
 OTHER INFORMATION: 42 nucleotides modified
 OTHER INFORMATION: 5 in position 4 and A
 OTHER INFORMATION: In position 6 are unmodified 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777

```

FILING DATE: 04-AUG-1993
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
  LENGTH: 35 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: CUNA
ORIGINAL SOURCE:
ORGANISM: CWP132
US 08-591 498-21

Query Match: 44.3%, Score 14, E-Val: Length 35,
Best Local Similarity: 76.2%, Freq. NO. 3, 1e-03,
Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

CY 11 CAGAGAGATTGCTTC 26
DB 11 CAGAGATTGCTTCATT 11

RESULT 33
US-08-171-718-10/c
Sequence 10, Application US/08171718
Patent No. 5733863
GENERAL INFORMATION:
  APPLICANT: Trolater, James A.
  APPLICANT: MacCollin, Mia M.
  APPLICANT: Gussella, James F.
  TITLE OF INVENTION: Tumor Suppressor Gene Mollin and Uses
  TITLE OF INVENTION: thereof
  NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Sterne, Kessler, Goldstein & Fox
  STREET: 1100 New York Avenue, N.W., Suite 600
  CITY: Washington
  STATE: D.C.
  COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC DOS/MS-DOS
  SOFTWARE: Patcom Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/171,718
  FILING DATE: 22-DEC-1993
  CLASSIFICATION: 436
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/108,808
  FILING DATE: 19-AUG-1993
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/112,104
  FILING DATE: 25-FEB-1993
  PRICE APPLICATION DATA:
  APPLICATION NUMBER: US 08/067,044
  FILING DATE: 04-MAR-1993
  ATTORNEY/AGENT INFORMATION:
  NAME: Brown, Anne
  REGISTRATION NUMBER: 36,463
  REFERENCE/POCKET NUMBER: 0809, 3850003
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 371-2500
  TELEFAX: (202) 371-2540
  INFORMATION FOR SEQ ID NO: 10:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 21 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
US 08 171-718-10
Query Match: 42.7%, Score 12.8, E-Val: Length 21,

```

```

Best Local Similarity: 87.5%, Freq. No. 3, 4e-03,
Matches: 14; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

CY 11 CAGAGAGATTGCTTC 26
DB 20 CAGAGGATTGCTTC 5

RESULT 34
US-08-478-087-10/c
Sequence 10, Application US/08478087
Patent No. 607685
GENERAL INFORMATION:
  APPLICANT: Trolater, James A.
  APPLICANT: MacCollin, Mia M.
  APPLICANT: Gussella, James F.
  TITLE OF INVENTION: Tumor Suppressor Gene Mollin and Uses
  TITLE OF INVENTION: thereof
  NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Sterne, Kessler, Goldstein & Fox
  STREET: 1100 New York Avenue, N.W., Suite 600
  CITY: Washington
  STATE: D.C.
  COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC DOS/MS-DOS
  SOFTWARE: Patcom Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/478,087
  FILING DATE: 07-JUN-1995
  CLASSIFICATION: 530
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/171,718
  FILING DATE: 22-DEC-1993
  APPLICATION NUMBER: US 08/108,808
  FILING DATE: 19-AUG-1993
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/112,104
  FILING DATE: 25-FEB-1993
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/067,044
  FILING DATE: 04-MAR-1993
  ATTORNEY/AGENT INFORMATION:
  NAME: Brown, Anne
  REGISTRATION NUMBER: 36,463
  REFERENCE/POCKET NUMBER: 0809, 3850003
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 371-2500
  TELEFAX: (202) 371-2540
  INFORMATION FOR SEQ ID NO: 10:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 21 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
US-08-478-087-10
Query Match: 42.7%, Score 12.8, E-Val: Length 21,
Best Local Similarity: 87.5%, Freq. No. 3, 4e-03,
Matches: 14; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

CY 11 CAGAGAGATTGCTTC 26
DB 20 CAGAGGATTGCTTC 5

RESULT 35
US-08-870-930-58
Sequence 58, Application US/08089300

```

CITY: King of Prussia
STATE: PA
COUNTRY: United States of America
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ 1.0, Version #1.05
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/08/591,498
FILING DATE: 25 SEPT 1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 15,467,153
FILING DATE: 2 JUL 1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/020,513
FILING DATE: 19 MAR 1997
AFFILIATION NUMBER: 600033,604
FILING DATE: 17 DEC 1997
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,964
REFERENCE TO SET NUMBER: A73,003-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5219
TELEFAX: 610 270 4926
TELEX:
INFORMATION FOR SET NO. 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US 09 939 5488 16

Query Match: 43.38; Score 13; DB 4; Length 23;
Best local similarity: 76.28; Pct. ID: 2.80%;
Matches: 16; Consistency: 0; Mismatches: 5; Indels: 0

CY 10 GCAGAGAAATGCTGTC 40
DB 22 GCGAGAAAGAGCTGTC 2

RESULT 31
US 09 939 5488 16
Sequence 16, Affiliation: 09/08/591,498
Patent No. 633994
GENERAL INFORMATION:
APPLICANT: Yanagisawa, Masashi
APPLICANT: Bergsma, Dirk
APPLICANT: Wilson, Shelagh
APPLICANT: Brooker, David
APPLICANT: Gellat, Miles
TITLE OF INVENTION: NEWEL LIGANDS OF THE NUCLEOSPTIDE
NUMBER OF INVENTION: RECEIVED HIGASHI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: United States of America
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: 09/08/591,498
FILING DATE: 26 SEPT 1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/08/591,498
FILING DATE: 2 JUL 1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/020,513
FILING DATE: 19 MAR 1997
AFFILIATION NUMBER: 600033,604
FILING DATE: 17 DEC 1997
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,964
REFERENCE TO SET NUMBER: A73,003-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5219
TELEFAX: 610 270 4926
TELEX:
INFORMATION FOR SET NO. 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US 09 939 5488 16

Query Match: 43.38; Score 13; DB 4; Length 23;
Best local similarity: 76.28; Pct. ID: 2.80%;
Matches: 16; Consistency: 0; Mismatches: 5; Indels: 0

CY 10 GCAGAGAAATGCTGTC 30
DB 22 GCGAGAAAGAGCTGTC 2

RESULT 32
US 09 939 5488 16
Sequence 16, Affiliation: 09/08/591,498
Patent No. 633994
GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMME, BRUNO P.A.
APPLICANT: REES, SARAH P.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: JOHANN DAHL & JOHANN
ADRESSEE: FRIEDRICH MACHION & SUTRO LUP
CITY: 1100 New York Avenue, N.W.
STATE: Washington
D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/08/591,498
FILING DATE: 25 JAN 1996
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/020,513
FILING DATE: 19 MAR 1997
AFFILIATION NUMBER: 600033,604
FILING DATE: 17 DEC 1997
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,964
REFERENCE TO SET NUMBER: A73,003-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5219
TELEFAX: 610 270 4926
TELEX:
INFORMATION FOR SET NO. 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US 09 939 5488 16

TITLE OF INVENTION: leeches.
 NUMBER OF SEQUENCES: 23
 INVENTOR: Kell & Weinlauf
 ADDRESS: 1101 Connecticut Avenue
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5 1/4 inch, 360 KB storage
 COMPUTER: IBM AT-compatible, 286K processor
 OPERATING SYSTEM: MS-DOS version 5.0
 SOFTWARE: WordPerfect version 5.1
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: US/08/444,114
 FILING DATE:
 CLASSIFICATION: 93C
 CLASSIFICATION: C07K 73/10
 CLASSIFICATION: A61K 37/54
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP92/02661
 FILING DATE: 19-NOV-1992
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-244-114.14

Query Match 44.7% Score 13.4 DB 1 Length 23
 Best Local Similarity 54.5% Pctd No. 1,944,033
 Matches 12, Conservative 0, Mismatches 4, Indels 0, Gaps 0

Qy 1 ATATTGGGCAAGAAATAT 22
 |||||
 Db 2 GCAATCTAAGAAATAT 23

RESULT 28
 US-09-311-260-125/c
 Sequence 11, Affiliation: US/09/311-260-125
 Patent No. 6214555
 GENERAL INFORMATION:
 APPLICANT: Leachman, James
 APPLICANT: Hull, May
 APPLICANT: Dunn, James M.
 TITLE OF INVENTION: METHOD FOR IDENTIFYING AND SELECTING ANTI-PT P-SELECTIN AG
 TITLE OF INVENTION: METHOD FOR IDENTIFYING AND SELECTING ANTI-PT P-SELECTIN AG
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Oppenahl & Larson LLP
 STREET: P.O. Box 5270
 CITY: Frisco
 STATE: CO
 COUNTRY: US
 ZIP: 80441-5270
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5 1/4 inch, 360 KB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: US/09/311,260
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 INFORMATION FOR SEQ ID NO: 21
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MODECODE TYPE: other nucleic acid
 HYPERHETICAL: no
 ANTI SENSE: no
 FRAGMENT TYPE: internal
 US-09-311-260-125

NAME: Larson, Marina T.
 REGISTRATION NUMBER: 72,038
 REFERENCE/PATENT NUMBER: US/09-890-363-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (970) 668-2083
 TELEFAX: (970) 668-2082
 TELEX:
 INFORMATION FOR SEQ ID NO: 125:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MODECODE TYPE: other nucleic acid
 HYPERHETICAL: no
 ANTI SENSE: no
 FRAGMENT TYPE: internal
 US-09-311-260-125

Query Match 44.7% Score 13.4 DB 4 Length 25
 Best Local Similarity 52.3% Pctd No. 1,944,033
 Matches 14, Conservative 0, Mismatches 1, Indels 0, Gaps 0

Qy 13 AAAAAATTTTCT 27
 |||||
 Db 24 AAAAAATTTTCT 10

RESULT 29
 US-09-484-617-43
 Sequence 43, Affiliation: US/09/484-617
 Patent No. 6103374
 GENERAL INFORMATION:
 APPLICANT: Herz, Chaz
 APPLICANT: Lex M. Cowsett
 TITLE OF INVENTION: ANTISENSE MEDIATION OF CASPASE EXPRESSION
 FILE REFERENCE: PUS-0103
 CURRENT APPLICATION NUMBER: US/09/484,617
 CURRENT FILING DATE: 2000-01-18
 NUMBER OF SEQ ID NOS: 176
 SEQ ID NO 43
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Artificial Sequence
 US-09-484-617-43

Query Match 44.0% Score 12.7 DB 4 Length 20
 Best Local Similarity 48.0% Pctd No. 1,944,033
 Matches 15, Conservative 0, Mismatches 3, Indels 0, Gaps 0

Qy 1 ATTTGGGCAAGAAATAT 23
 |||||
 Db 3 ATTTGGGCAAGAAATAT 20

RESULT 30
 US-08-938-548B-16/c
 Sequence 16, Affiliation: US/08/938-548B-16
 Patent No. 6001963
 GENERAL INFORMATION:
 APPLICANT: Yamaizawa, Masashi
 APPLICANT: Bergsma, Dirk
 APPLICANT: Wilson, Sheldagh
 APPLICANT: Brooks, David
 APPLICANT: Galina, Mikha
 TITLE OF INVENTION: NOVEL LIGANDS OF THE NEUROPEPTIDE
 TITLE OF INVENTION: PEPTIDE HEPATITIS
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 1515 Swedeland Road

```

REFERENCE/DOCKET NUMBER: NEXA1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 5'-phosphorylated
FEATURe:
OTHER INFORMATION: N at position 10 is a 5'-linked deoxythymidine
OTHER INFORMATION: 3'-3' linked deoxythymidine
US-09-870-930-55

Query Match: 46.0%, Score 13.8, Pos 4, Length 30
Best local similarity: 70.6%, Pos 1, No. 13e-03
Matches: 10, Mismatches: 3, Indels: 0, Gaps: 0

CY 6 TGGGCAAGAGATG 22
DE 6 TGGGCAAGAGATG 22

RESULT 25
US-09-254-968-59
Sequence 59, Application US/0924968
Patent No. 6426336
GENERAL INFORMATION:
APPLICANT: NEXA1, BARRY D. SWANSON, CHANNA VAN HEELE, MICHAEL WILLIS
TITLE OF INVENTION: Amino acid sequence
NUMBER OF SEQUENCES: 1
REFERENCE ADDRESS:
ADDRESSER: Swanson and Proffitt, LLC
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Magnetic, 3 1/2 inch, 14 MB storage
COMMENTS: IBM compatible
(C) OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09254968
FILING DATE: 13-Mar-2000
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09254968
FILING DATE: 13-Mar-2000
APPLICATION NUMBER: US/09254968
FILING DATE: 25-OCTOBER-1996
APPLICATION NUMBER: US/09254968
FILING DATE: 6-JUNE-1997
APPLICATION NUMBER: US/09254968
FILING DATE: 21-JULY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry D. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXA1/09254968
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 59
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid

```

```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-phosphorylated
FEATURe:
OTHER INFORMATION: N at position 10 is a 5'-linked deoxythymidine
SEQUENCE INFORMATION: SEQ ID NO: 59
US-09-254-968-59

Query Match: 46.0%, Score 13.8, Pos 4, Length 30
Best local similarity: 70.6%, Pos 1, No. 13e-03
Matches: 10, Mismatches: 3, Indels: 0, Gaps: 0

CY 6 TGGGCAAGAGATG 22
DE 6 TGGGCAAGAGATG 22

RESULT 26
US-09-540-014-8/C
Sequence 8, Application US/09540014
Patent No. 6380372
GENERAL INFORMATION:
APPLICANT: Cho, Myoung-Je
APPLICANT: Del Val, Greg
APPLICANT: Caliau, Maxime
APPLICANT: Lemay, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Baiter gene for Mycobacterium and
FILE OF INVENTION: N/A
FILE REFERENCE: 2001-0701130
CURRENT APPLICATION NUMBER: US/09540014
PRIOR APPLICATION NUMBER: US/00031198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US/00031198
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US/00031198
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/00031198
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FASTA for Windows Version 4.0
SEQ ID NO: 8
LENGTH: 34
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-540-014-8

Query Match: 46.0%, Score 13.8, Pos 4, Length 34
Best local similarity: 70.6%, Pos 1, No. 13e-03
Matches: 10, Mismatches: 3, Indels: 0, Gaps: 0

CY 34 ATTGGGCAAGAGATG 28
DE 34 ATTGGGCAAGAGATG 28

RESULT 27
US-09-244-113-14
Sequence 14, Application US/09244113
Patent No. 5456181
GENERAL INFORMATION:
APPLICANT: Strube, Karl-Hermann
APPLICANT: Bialojan, Siegfried
APPLICANT: Krieger, Burkard
APPLICANT: Friedrich, Thomas
TITLE OF INVENTION: No. 5456181: Inhibitor-antibiotic resistance gene

```


STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 13-Mar-2000
 CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 13-Mar-2000
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 25-October-1996
 APPLICATION NUMBER: 08/09/1996
 FILING DATE: 6-June-1997
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 21-July-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 FILING DATE: 13-Mar-2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA

FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
 modified

FEATURE:
 OTHER INFORMATION: Further are 2' (methoxy) (2'-OMe) modified

FEATURE:
 OTHER INFORMATION: 2 in position 10, A in position 12, and G in position 22 are unmodified (1-F, 2'-OH)

SEQUENCE DESCRIPTION: SEQ ID NO: 781
 US-09-254 960 70

Query Match 46.0% Score 13.87 DR 4 Length 197
 Best Local Similarity 70.6% Pred. No. 1.3e+03
 Matches 12, Conservative 3, Mismatches 2, Inbels 0, Gaps 0

US-09-254 960 70

6 TGGCGCAAGAGAAATG 22
 ||||| |||||
 6 TGGCGGAGAGAAATG 22

RESULT 21
 US-09-254 960 70
 Sequence 70, Affiliation 18/09/1996
 Patent No. 6426335

GENERAL INFORMATION:
 APPLICANT: MICHAEL WILLIS
 TITLE OF INVENTION: VASCULAR ENDOTHelial GROWTH FACTOR (VEGF) INHIBITOR
 ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Ratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 13-Mar-2000
 CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 13-Mar-2000
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 25-October-1996
 APPLICATION NUMBER: 08/09/1996
 FILING DATE: 6-June-1997
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 21-July-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 FILING DATE: 13-Mar-2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA

FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
 modified

FEATURE:
 OTHER INFORMATION: Further are 2' (methoxy) (2'-OMe) modified

FEATURE:
 OTHER INFORMATION: G in position 10 and A in position 12 are unmodified (1-F, 2'-OH)

SEQUENCE DESCRIPTION: SEQ ID NO: 782
 US-09-254 968 79

Query Match 46.0% Score 13.87 DR 4 Length 197
 Best Local Similarity 70.6% Pred. No. 1.3e+03
 Matches 12, Conservative 3, Mismatches 2, Inbels 0, Gaps 0

US-09-254 968 79

6 TGGCGCAAGAGAAATG 22
 ||||| |||||
 6 TGGCGGAGAGAAATG 22

RESULT 22
 US-09-254 968 80
 Sequence 70, Affiliation 18/09/1996
 Patent No. 6426335

GENERAL INFORMATION:
 APPLICANT: MICHAEL WILLIS
 TITLE OF INVENTION: VASCULAR ENDOTHelial GROWTH FACTOR (VEGF) INHIBITOR
 ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Ratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible

OTHER INFORMATION: All pyrimidines are 2'-fluoro
FEATURE:
OTHER INFORMATION: Purines are 2'-O-methyl
OTHER INFORMATION: (2' OMe) modified
FEATURE:
OTHER INFORMATION: G in position 10 and A in
OTHER INFORMATION: position 12 are unmodified (i.e., 2' OH)
US-09-870-930-75

Query March 46.0% Score 13.8; DB 4; Length 29;
Best Local Similarity 70.6% Prod No 13663;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

DB 6 TGGGACAGCAATG 22
6 TGGGACAGCAATG 22

RESULT 18
US-09-870-930-76

Sequence 76, Application US/04470930
Patent No. 6168778
GENERAL INFORMATION
APPLICANT: NEBOJSA JANDIC, LARRY GOLD, PAUL G. SCHMITZ, CHANDRA VAN DERSE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
TITLE OF INVENTION: VEGF-A-10 LIGAND ANALOGUES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WinPerfect 9.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/04470930
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION
NAME: Ravi J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433

OTHER INFORMATION: A in position 12 and G
OTHER INFORMATION: in position 22 are unmodified (i.e., 2' OH)
US-09-870-930-76

LENGTH: 29
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
FEATURE:
OTHER INFORMATION: Purines are 2' O-methyl
OTHER INFORMATION: (2' OMe) modified
FEATURE:
OTHER INFORMATION: G in position 12 and G in
OTHER INFORMATION: position 22 are unmodified (i.e., 2' OH)
US-09-870-930-76

Query March 46.0% Score 13.8; DB 4; Length 29;
Best Local Similarity 70.6% Prod No 13663;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

DB 6 TGGGACAGCAATG 22
6 TGGGACAGCAATG 22

DB 6 TGGGACAGCAATG 22
6 TGGGACAGCAATG 22

RESULT 19
US-09-870-930-77

Sequence 77, Application US/04470930
Patent No. 6168778
GENERAL INFORMATION
APPLICANT: NEBOJSA JANDIC, LARRY GOLD, PAUL G. SCHMITZ, CHANDRA VAN DERSE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
TITLE OF INVENTION: VEGF-A-10 LIGAND ANALOGUES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WinPerfect 9.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/04470930
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Ravi J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433

OTHER INFORMATION: A in position 12 and G
OTHER INFORMATION: in position 22 are unmodified (i.e., 2' OH)
US-09-870-930-77

LENGTH: 29
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
FEATURE:
OTHER INFORMATION: Purines are 2' O-methyl
OTHER INFORMATION: (2' OMe) modified
FEATURE:
OTHER INFORMATION: A in position 12 and G
OTHER INFORMATION: in position 22 are unmodified (i.e., 2' OH)
US-09-870-930-77

Query March 46.0% Score 13.8; DB 4; Length 29;
Best Local Similarity 70.6% Prod No 13663;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

DB 6 TGGGACAGCAATG 22
6 TGGGACAGCAATG 22

RESULT 20
US-09-254-968-78

Sequence 78, Application US/0113168
Patent No. 642635
GENERAL INFORMATION
APPLICANT: NEBOJSA JANDIC, LARRY GOLD, PAUL G. SCHMITZ, CHANDRA VAN DERSE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
TITLE OF INVENTION: VEGF-A-10 LIGAND ANALOGUES
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.

```

NAME: Barry J. Swanson
REGISTRATION NUMBER: 92,215
REFERENCE/TOKENET NUMBER: NEW61
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (303) 793-3333
    TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 29
TYPE: nucleic acid
SYNADDRESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: A, G pyrimidines are
OTHER INFORMATION: 2, C, U, G modified
FEATURE: OTHER INFORMATION: P, Q, Y, R, S, T, V, W, X, Z, [ ] modified
OTHER INFORMATION: 8 in position 19, A in position 10
OTHER INFORMATION: 8 in position 22 are unmodified 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29
Query Match          46.0% Score 13.8; DH 4; Length 29;
Best Local Similarity 70.6%; Pred No. 1,3e+03;
Matches   12; Conservative   3; Mismatches   2; Indels   0; gaps   0
Cy         6 TCAGGAAAGAATGG 22
Db         6 TGCGAAGGAATAUG 22

RESULT 17
Sequence no: Affiliation: Parent No.:
GENERAL INFORMATION:
AFFILIATION: HELMUT-A. JANZIG, CARL LUDWIG PAULSEN, HANNOVER UNIVERSITY OF MEDICINE AND PHYSIOLOGICAL CHEMISTRY, LEIBNIZ-INSTITUT FUR MOLECULAR ENDOCRINOLOGY, DEPT. B, D-30559 HARBURG, FRANKRICH
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTORS
TITLE OF INVENTION: NUCLEAR ACID LIQUID COMPLEXES
NUMBER OF SEQUENCES: 88
CORRESPONDING ADDRESS:
ADDRESSEE: Swanson & Bratschan, L.P.C., STREET: 8400 East Prentice Avenue, Suite #200 CITY: Denver STATE: Colorado COUNTRY: USA ZIP: 80111
COMPUTER READABLE FORM:
MEDIA TYPE: Diskette, 3.5 inch, 1.4 Mb storage
OPERATING SYSTEM: IBM compatible
SOFTWARE: Watson v. 8.0
SUBJECT AREA/DISEASE DATA:
AFFILIATED NUMBER: US 6,900,930
PILING DATE: 6 June 1997
CLASSIFICATION: B3E
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/TOKENET NUMBER: NEW61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 29
TYPE: nucleic acid
STRANDS/SUBST: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:

```

Query Match 46.0% Score 13.8; DB 4; Length 28;
Best Local Similarity 70.4% Ptd No. 13-033;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

QY 6 TGGGAGAGAGATG 22
|||||
DB 6 UGGGAGAGAGATG 22

RESULT 13
US-09-870-930-57

Sequence 57, Application US/09870930

Patent No. 6168778

GENERAL INFORMATION:

APPLICANT: NEBOSA JANIC, LARRY GOLD, PAUL G. STIMMIT, CHANDRA VAPPESE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

TITLE OF INVENTION: NUCLEIC ACID LIGAND COMPLEXES

NUMBER OF SEQUENCES: 08

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.

STREET: 8400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER PEAKABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: Windows

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09870930

FILING DATE: 6 JUNE 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,015

REFERENCE/DOCKET NUMBER: NEX-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3333

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2'-fluoro

OTHER INFORMATION: 5' to 3' direction is 5' to 3'

US-09-870-930-57

Query Match 46.0% Score 13.8; DB 4; Length 28;

Best Local Similarity 70.4% Ptd No. 13-033;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

QY 6 TGGGAGAGAGATG 22

|||||

DB 6 UGGGAGAGAGATG 21

RESULT 14

US-09-254-968-60

Sequence 57, Application US/09254968

Patent No. 6426335

GENERAL INFORMATION:

APPLICANT: NEBOSA JANIC, LARRY GOLD, PAUL G. STIMMIT, CHANDRA VAPPESE,

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NUCLEIC

ACID LIGAND COMPLEXES

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.

STREET: 8400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER PEAKABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

(C) OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09254968

FILING DATE: 13 MAR 2000

CLASSIFICATION: 536

FILED APPLICATION DATA:

APPLICATION NUMBER: US/09254968

FILING DATE: 17 OCTOBER 1997

APPLICATION NUMBER: 08/739,109

FILING DATE: 25 OCTOBER 1996

APPLICATION NUMBER: 08/870,930

FILING DATE: 6 JUNE 1997

APPLICATION NUMBER: 08/857,351

FILING DATE: 21 JULY 1997

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,015

REFERENCE/DOCKET NUMBER: NEX-1/PRT 03

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3333

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2'-fluoro

OTHER INFORMATION: modified

US-09-254-968-60

Query Match 46.0% Score 13.8; DB 4; Length 28;

Best Local Similarity 70.4% Ptd No. 13-033;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

QY 6 TGGGAGAGAGATG 22

|||||

DB 6 UGGGAGAGAGATG 22

RESULT 15

US-09-254-968-61

Sequence 57, Application US/09254968

Patent No. 6426335

GENERAL INFORMATION:

APPLICANT: NEBOSA JANIC, LARRY GOLD, PAUL G. STIMMIT, CHANDRA VAPPESE,

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NUCLEIC

ACID LIGAND COMPLEXES

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.

STREET: 8400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER PEAKABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

CV 6 TCGGCGACAGAGAA 19
DB 30 TCGGCGACAGAGAA 17

RESULT 10

US-09-562-868-14/C
Sequence 14, Alignment 14, Score 14, DB 4, Length 32
Patent No. 6432680
GENERAL INFORMATION:
APPLICANT: Liao, Yao Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6432680
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
FIELD REFERENCE: 22000 000702 02/04/97, etc
CURRENT APPLICATION NUMBER: 09/090,693
CURRENT FILING DATE: 2000-03-31
PRIORITY APPLICATION NUMBER: 60/390,093
PRIORITY FILING DATE: 1998-03-31
PRIORITY APPLICATION NUMBER: 09/090,693
PRIORITY FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: Sequence alignment with which it is related
OTHER INFORMATION: Proteins through the cell membrane into the cell
PUBLICATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-562-868-14

Query Match 46.7%, Score 14, DB 4, Length 32
Best Local Similarity 100.0%, From 14, 11e+03
Matches 14, Conservation of Mutations of Indels 0, Gaps 0

CV 6 TCGGCGACAGAGAA 19
DB 30 TCGGCGACAGAGAA 20

RESULT 11

US-09-562-868-18/C
Sequence 18, Alignment 18, Score 18, DB 4, Length 32
Patent No. 6432680
GENERAL INFORMATION:
APPLICANT: Lin, Yao Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6432680
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
FIELD REFERENCE: 22000 000702 02/04/97, etc
CURRENT APPLICATION NUMBER: 09/090,693
CURRENT FILING DATE: 2000-03-31
PRIORITY APPLICATION NUMBER: 60/390,093
PRIORITY FILING DATE: 1998-03-31
PRIORITY APPLICATION NUMBER: 09/090,693
PRIORITY FILING DATE: 1998-11-04

NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: Sequence alignment with which it is related
OTHER INFORMATION: Proteins through the cell membrane into the cell
PUBLICATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-562-868-19

Query Match 46.7%, Score 14, DB 4, Length 32
Best Local Similarity 100.0%, From 14, 11e+03
Matches 14, Conservation of Mutations of Indels 0, Gaps 0

CV 6 TCGGCGACAGAGAA 19
DB 30 TCGGCGACAGAGAA 17

RESULT 12

US-09-870-930-56
Sequence 56, Alignment 56, Score 56, DB 4, Length 32
Patent No. 6432680
GENERAL INFORMATION:
APPLICANT: HERSCA CARLOS, LARRY GARY, PAUL J. JOHNSON, THOMAS W. JOHNSON, M. J. JOHNSON
TITLE OF INVENTION: "VASCULAR ENDOTHELIAL GROWTH FACTOR VEGF
TITLE OF INVENTION: "VEGF AND ITS ANALOGS IN TISSUE REPAIR"
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson and Blatschun, L.L.C.
STREET: 4400 First Service Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
CONTACT FEATURES: ELEM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/090,693
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Carlson
REGISTRATION NUMBER: 33,215
REFERENCE/JUDICIAL NUMBER: NEX01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All primers are 2' fluoro

Best Local Similarity: 100.0%, Score 14, Length 33,
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCGGCGACAGAGAA 19
DB 27 TCGGCGACAGAGAA 14

```

RESULT 7
US-09-186-170-14
Sequence 14, Application US/03/186170
Patent No. 6248598
GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6432680
TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: 22000.009702
CURRENT APPLICATION NUMBER: US/03/186170
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US/98-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 09/186,170
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 17
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: Sequence encoding peptide which transports
OTHER INFORMATION: Proteins through the cell membrane into the cell
EXPLANATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: "Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-186-170-14

```

Query Match 46.7%, Score 14, DB 4, Length 33,
Best Local Similarity: 100.0%, Score 14, Length 33,
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCGGCGACAGAGAA 19
DB 27 TCGGCGACAGAGAA 14

```

RESULT 8
US-09-186-170-14
Sequence 14, Application US/03/186170
Patent No. 6248598
GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248598
TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: US/98-03-31
CURRENT APPLICATION NUMBER: US/03/186170
CURRENT FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 09/186,170
PRIOR FILING DATE: 1998-11-04

```

FASTA FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 14
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: Sequence encoding peptide which transports
OTHER INFORMATION: Proteins through the cell membrane into the cell
EXPLANATION INFORMATION:
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: "Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
RELEVANT RESOURCES: 1 TO 12
US-09-186-170-14

Query Match 46.7%, Score 14, DB 4, Length 33,
Best Local Similarity: 100.0%, Score 14, Length 33,
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCGGCGACAGAGAA 19
DB 33 TCGGCGACAGAGAA 20

```

RESULT 9
US-09-186-170-18/C
Sequence 18, Application US/03/186170
Patent No. 6248598
GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248598
TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: US/98-03-31
CURRENT APPLICATION NUMBER: US/03/186170
CURRENT FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US/98-03-31
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 18
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: Sequence encoding peptide which transports
OTHER INFORMATION: Proteins through the cell membrane into the cell
EXPLANATION INFORMATION:
TITLE: "Genetic Engineering of Proteins with Cell Membrane  
TITLE: "Permeability"  
JOURNAL: Nature Biotechnology  
VOLUME: 16  
ISSUE: April  
PAGES: 370-375  
DATE: 1998-04-01  
RELEVANT RESOURCES: 1 TO 12  
US-09-186-170-18

```

Query Match 46.7%, Score 14, DB 4, Length 33,
Best Local Similarity: 100.0%, Score 14, Length 33,
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09 562 966 15

Query Match: 46.73, Score 14, DB 4, Length 24,
 Best Local Similarity: 100.0%, Filed No. 1998-03-21
 Matches: 14, Conserved: 0, Mismatched: 0, 16 bits 0, 34%

CY 6 TGGCGCAGAGAGAA 19

DB 24 TGGCGCAGAGAGAA 8

RESULT 4

US-09 562 966 15

Sequence 16, Applicant: "Genetic Engineering"

Patent No. 6248558

GENERAL INFORMATION:

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of"

Patent No. 6248558

TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"

FILE REFERENCE: V09641

CURRENT APPLICATION NUMBER: US/09/186,170

CURRENT FILING DATE: 1998-11-04

EARLIER APPLICATION NUMBER: 1998-03-21

EARLIER FILING DATE: 1998-03-21

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding protein which transports

OTHER INFORMATION: Protein through the cell membrane into the cell

PUBLICATION INFORMATION:

TITLE: "Genetic Engineering of Proteins with Cell Membrane

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-375

DATE: 1998-04-01

RELEVANT RESIDUES: 1 TO 12

US-09 186 170 16

Query Match:

46.73, Score 14, DB 1, Length 27,

Best Local Similarity: 100.0%, Filed No. 1998-03-21

Matches: 14, Conserved: 0, Mismatched: 0, 16 bits 0,

CY 6 TGGCGCAGAGAGAA 19

DB 24 TGGCGCAGAGAGAA 11

RESULT 5

US-09 562 966 15

Sequence 16, Applicant: "Genetic Engineering"

Patent No. 6248558

GENERAL INFORMATION:

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of"

Patent No. 6248558

TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"

FILE REFERENCE: 4200000000

CURRENT APPLICATION NUMBER: US/09/186,170

CURRENT FILING DATE: 1998-03-21

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding protein which transports

OTHER INFORMATION: Protein through the cell membrane into the cell

PUBLICATION INFORMATION:

TITLE: "Genetic Engineering of Proteins with Cell Membrane

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-375

DATE: 1998-04-01

RELEVANT RESIDUES: 1 TO 12

US-09 186 170 17

Query Match:

46.73, Score 14, DB 4, Length 27,

Best Local Similarity: 100.0%, Filed No. 1998-03-21

Matches: 14, Conserved: 0, Mismatched: 0, 16 bits 0, 34%

FIRST APPLICATION NUMBER: 62/060,083

PRIORITY FILING DATE: 1998-03-21

FIRST APPLICATION NUMBER: 187156,170

PRIORITY FILING DATE: 1998-11-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding protein which transports

OTHER INFORMATION: Protein through the cell membrane into the cell

PUBLICATION INFORMATION:

TITLE: "Genetic Engineering of Proteins with Cell Membrane

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-375

DATE: 1998-04-01

US-09 562 966 16

Query Match:

46.73, Score 14, DB 4, Length 27,

Best Local Similarity: 100.0%, Filed No. 1998-03-21

Matches: 14, Conserved: 0, Mismatched: 0, 16 bits 0, 34%

CY 6 TGGCGCAGAGAGAA 19

DB 24 TGGCGCAGAGAGAA 11

RESULT 6

US-09 562 966 15

Sequence 16, Applicant: "Genetic Engineering"

Patent No. 6248558

GENERAL INFORMATION:

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of"

Patent No. 6248558

TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"

FILE REFERENCE: V09641

CURRENT APPLICATION NUMBER: US/09/186,170

CURRENT FILING DATE: 1998-11-04

EARLIER APPLICATION NUMBER: 1998-03-21

EARLIER FILING DATE: 1998-03-21

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 17

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding protein which transports

OTHER INFORMATION: Protein through the cell membrane into the cell

PUBLICATION INFORMATION:

TITLE: "Genetic Engineering of Proteins with Cell Membrane

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-375

DATE: 1998-04-01

RELEVANT RESIDUES: 1 TO 12

US-09 186 170 17

Query Match:

46.73, Score 14, DB 4, Length 30,

Best Local Similarity: 100.0%, Filed No. 1998-03-21

Matches: 14, Conserved: 0, Mismatched: 0, 16 bits 0, 34%

```

977 10.2 34.0 30 4 US-09-037-192-19 Sequence 39, Appl
C 978 10.2 34.0 30 4 US-09-216-288-24 Sequence 34, Appl
C 979 10.2 34.0 30 4 US-09-401-474-54 Sequence 54, Appl
980 10.2 34.0 30 4 US-09-628-490-24 Sequence 32, Appl
C 981 10.2 34.0 31 1 US-07-921-7178-1 Sequence 1, Appl
C 982 10.2 34.0 31 1 US-07-779-464-1 Sequence 1, Appl
C 983 10.2 34.0 31 1 US-08-119-262B-1 Sequence 1, Appl
C 984 10.2 34.0 31 1 US-08-446-486-27 Sequence 27, Appl
C 985 10.2 34.0 31 1 US-08-135-929A-1 Sequence 1, Appl
C 986 10.2 34.0 31 1 US-06-234-265A-1 Sequence 1, Appl
C 987 10.2 34.0 31 1 US-08-463-308-27 Sequence 27, Appl
C 988 10.2 34.0 31 1 US-08-463-308-27 Sequence 27, Appl
C 989 10.2 34.0 31 1 US-09-142-982-34 Sequence 89, Appl
C 990 10.2 34.0 31 1 US-09-142-982-34 Sequence 89, Appl
C 991 10.2 34.0 31 2 US-08-739-167-84 Sequence 89, Appl
C 992 10.2 34.0 31 3 US-09-404-796-84 Sequence 89, Appl
C 993 10.2 34.0 31 3 US-09-931-869-84 Sequence 89, Appl
C 994 10.2 34.0 31 3 US-08-578-686C-5 Sequence 89, Appl
C 995 10.2 34.0 31 4 US-09-094-485-5 Sequence 89, Appl
996 10.2 34.0 31 3 US-09-410-832-54 Sequence 89, Appl
C 997 10.2 34.0 31 3 US-09-009-913-199 Sequence 199, Appl
C 998 10.2 34.0 31 3 US-09-144-112-5 Sequence 5, Appl
C 999 10.2 34.0 31 4 US-08-895-981-5 Sequence 5, Appl
C1000 10.2 34.0 31 4 US-09-450-444-54 Sequence 89, Appl

```

ALIGNMENTS

RESULT 1

```

US-09-257-544-11/c
Sequence 14, Application US/09257584A
Patent No. 6197611

```

```

GENERAL INFORMATION:
APPLICANT: Rice, Douglas A.
TITLE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 7719 31, 09/04/19701A
CURRENT APPLICATION NUMBER: 09/0257584A
PRIORITY FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 09/060490
EARLIER FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 13
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Maize
OTHER INFORMATION: gene specific for primer
US-09-257-544-11

```

```

Query Match 47 38 Score 14.2 (16.4) Length 27;
Best Local Similarity 94.28 (96.1) Pos: 8,561/72;
Matches 16, Conservative 0, Mismatches 3, Indels 0, Gaps 0

```

```

UY 1 GTATTGCGAGAGAA 19
DB 20 GAAAGTGGGAGAGATA 2

```

```

RESULT 2
US-09-186-170-15/c
Sequence 14, Application US/09186170
Patent No. 6248548
GENERAL INFORMATION:
APPLICANT: Tan, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248548
TITLE OF INVENTION: "Protein with Cell Membrane Translocating Activity"

```

```

FILE REFERENCE: US9841
CURRENT APPLICATION NUMBER: US/09186170
PRIORITY FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 08/056,083
PRIORITY FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 15
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nuclear rib
OTHER INFORMATION: Sequence encoding protein which transpor
OTHER INFORMATION: Protein through the cell membrane into the cell
OTHER INFORMATION:
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: "Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
RELEVANT RESIDUES: 1 TO 12
US-09-186-170-15

```

Query Match

```

Best Local Similarity 100.08 (100.08) Pred. No. 1e+01;
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0

```

```

UY 5 TGGGCGAGAGAA 19
DB 21 TGGGCGAGAGAA 8

```

RESULT 3

```

US-09-560-868-15/c
Sequence 15, Application US/09560868
Patent No. 6432660

```

```

GENERAL INFORMATION:
APPLICANT: Tan, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6432660
TITLE OF INVENTION: "Protein with Cell Membrane Translocating Activity"
FILE REFERENCE: 22099 09/0702
CURRENT APPLICATION NUMBER: 09/560868
PRIORITY FILING DATE: 2000-05-01
PRIORITY FILING DATE: 1998-03-31
PRIORITY FILING DATE: 1998-03-31
PRIORITY FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 15
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nuclear rib
OTHER INFORMATION: Sequence encoding protein which transpor
OTHER INFORMATION: Protein through the cell membrane into the cell
OTHER INFORMATION:
AUTHORS: Rojas, M et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01

```

[illegible]

685	10.4	34.7	22	1	US-09-890-363-1	Sequence 18, Affl
686	10.4	34.7	22	2	US-09-890-363-1	Sequence 21, Affl
687	10.4	34.7	22	3	US-09-890-363-1	Sequence 24, Affl
688	10.4	34.7	22	4	US-09-890-363-1	Sequence 27, Affl
689	10.4	34.7	22	5	US-09-890-363-1	Sequence 30, Affl
690	10.4	34.7	22	6	US-09-890-363-1	Sequence 33, Affl
691	10.4	34.7	22	7	US-09-890-363-1	Sequence 36, Affl
692	10.4	34.7	22	8	US-09-890-363-1	Sequence 39, Affl
693	10.4	34.7	22	9	US-09-890-363-1	Sequence 42, Affl
694	10.4	34.7	22	10	US-09-890-363-1	Sequence 45, Affl
695	10.4	34.7	22	11	US-09-890-363-1	Sequence 48, Affl
696	10.4	34.7	22	12	US-09-890-363-1	Sequence 51, Affl
697	10.4	34.7	22	13	US-09-890-363-1	Sequence 54, Affl
698	10.4	34.7	22	14	US-09-890-363-1	Sequence 57, Affl
699	10.4	34.7	22	15	US-09-890-363-1	Sequence 60, Affl
700	10.4	34.7	22	16	US-09-890-363-1	Sequence 63, Affl
701	10.4	34.7	22	17	US-09-890-363-1	Sequence 66, Affl
702	10.4	34.7	22	18	US-09-890-363-1	Sequence 69, Affl
703	10.4	34.7	22	19	US-09-890-363-1	Sequence 72, Affl
704	10.4	34.7	22	20	US-09-890-363-1	Sequence 75, Affl
705	10.4	34.7	22	21	US-09-890-363-1	Sequence 78, Affl
706	10.4	34.7	22	22	US-09-890-363-1	Sequence 81, Affl
707	10.4	34.7	22	23	US-09-890-363-1	Sequence 84, Affl
708	10.4	34.7	22	24	US-09-890-363-1	Sequence 87, Affl
709	10.4	34.7	22	25	US-09-890-363-1	Sequence 90, Affl
710	10.4	34.7	22	26	US-09-890-363-1	Sequence 93, Affl
711	10.4	34.7	22	27	US-09-890-363-1	Sequence 96, Affl
712	10.4	34.7	22	28	US-09-890-363-1	Sequence 99, Affl
713	10.4	34.7	22	29	US-09-890-363-1	Sequence 102, Affl
714	10.4	34.7	22	30	US-09-890-363-1	Sequence 105, Affl
715	10.4	34.7	22	31	US-09-890-363-1	Sequence 108, Affl
716	10.4	34.7	22	32	US-09-890-363-1	Sequence 111, Affl
717	10.4	34.7	22	33	US-09-890-363-1	Sequence 114, Affl
718	10.4	34.7	22	34	US-09-890-363-1	Sequence 117, Affl
719	10.4	34.7	22	35	US-09-890-363-1	Sequence 120, Affl
720	10.4	34.7	22	36	US-09-890-363-1	Sequence 123, Affl
721	10.4	34.7	22	37	US-09-890-363-1	Sequence 126, Affl
722	10.4	34.7	22	38	US-09-890-363-1	Sequence 129, Affl
723	10.4	34.7	22	39	US-09-890-363-1	Sequence 132, Affl
724	10.4	34.7	22	40	US-09-890-363-1	Sequence 135, Affl
725	10.4	34.7	22	41	US-09-890-363-1	Sequence 138, Affl
726	10.4	34.7	22	42	US-09-890-363-1	Sequence 141, Affl
727	10.4	34.7	22	43	US-09-890-363-1	Sequence 144, Affl
728	10.4	34.7	22	44	US-09-890-363-1	Sequence 147, Affl
729	10.4	34.7	22	45	US-09-890-363-1	Sequence 150, Affl
730	10.4	34.7	22	46	US-09-890-363-1	Sequence 153, Affl
731	10.4	34.7	22	47	US-09-890-363-1	Sequence 156, Affl
732	10.4	34.7	22	48	US-09-890-363-1	Sequence 159, Affl
733	10.4	34.7	22	49	US-09-890-363-1	Sequence 162, Affl
734	10.4	34.7	22	50	US-09-890-363-1	Sequence 165, Affl
735	10.4	34.7	22	51	US-09-890-363-1	Sequence 168, Affl
736	10.4	34.7	22	52	US-09-890-363-1	Sequence 171, Affl
737	10.4	34.7	22	53	US-09-890-363-1	Sequence 174, Affl
738	10.4	34.7	22	54	US-09-890-363-1	Sequence 177, Affl
739	10.4	34.7	22	55	US-09-890-363-1	Sequence 180, Affl
740	10.4	34.7	22	56	US-09-890-363-1	Sequence 183, Affl
741	10.4	34.7	22	57	US-09-890-363-1	Sequence 186, Affl
742	10.4	34.7	22	58	US-09-890-363-1	Sequence 189, Affl
743	10.4	34.7	22	59	US-09-890-363-1	Sequence 192, Affl
744	10.4	34.7	22	60	US-09-890-363-1	Sequence 195, Affl
745	10.4	34.7	22	61	US-09-890-363-1	Sequence 198, Affl
746	10.4	34.7	22	62	US-09-890-363-1	Sequence 201, Affl
747	10.4	34.7	22	63	US-09-890-363-1	Sequence 204, Affl
748	10.4	34.7	22	64	US-09-890-363-1	Sequence 207, Affl
749	10.4	34.7	22	65	US-09-890-363-1	Sequence 210, Affl
750	10.4	34.7	22	66	US-09-890-363-1	Sequence 213, Affl
751	10.4	34.7	22	67	US-09-890-363-1	Sequence 216, Affl
752	10.4	34.7	22	68	US-09-890-363-1	Sequence 219, Affl
753	10.4	34.7	22	69	US-09-890-363-1	Sequence 222, Affl
754	10.4	34.7	22	70	US-09-890-363-1	Sequence 225, Affl
755	10.4	34.7	22	71	US-09-890-363-1	Sequence 228, Affl
756	10.4	34.7	22	72	US-09-890-363-1	Sequence 231, Affl
757	10.4	34.7	22	73	US-09-890-363-1	Sequence 234, Affl

[illegible]

[illegible]

29	13.4	44.7	25	4	US-09-311-260-115	Sequence 13	At
28	13.4	44.7	24	4	US-08-939-548-16	Sequence 14	At
33	13	43.3	23	4	US-08-939-093A-16	Sequence 15	At
31	13	43.3	23	4	US-08-939-093A-16	Sequence 16	At
32	12.8	42.7	21	4	US-08-921-944-21	Sequence 17	At
34	12.8	42.7	21	4	US-08-921-944-21	Sequence 18	At
33	12.8	42.7	21	4	US-08-921-944-21	Sequence 19	At
35	12.4	42.7	21	4	US-08-921-944-21	Sequence 20	At
36	12.4	42.7	21	4	US-08-921-944-21	Sequence 21	At
37	12.4	42.7	21	4	US-08-921-944-21	Sequence 22	At
38	12.4	42.7	21	4	US-08-921-944-21	Sequence 23	At
39	12.4	42.7	21	4	US-08-921-944-21	Sequence 24	At
40	12.4	42.7	21	4	US-08-921-944-21	Sequence 25	At
41	12.4	42.7	21	4	US-08-921-944-21	Sequence 26	At
42	12.4	42.7	21	4	US-08-921-944-21	Sequence 27	At
43	12.4	42.7	21	4	US-08-921-944-21	Sequence 28	At
44	12.4	42.7	21	4	US-08-921-944-21	Sequence 29	At
45	12.4	42.7	21	4	US-08-921-944-21	Sequence 30	At
46	12.4	42.7	21	4	US-08-921-944-21	Sequence 31	At
47	12.4	42.7	21	4	US-08-921-944-21	Sequence 32	At
48	12.4	42.7	21	4	US-08-921-944-21	Sequence 33	At
49	12.4	42.7	21	4	US-08-921-944-21	Sequence 34	At
50	12.4	42.7	21	4	US-08-921-944-21	Sequence 35	At
51	12.4	42.7	21	4	US-08-921-944-21	Sequence 36	At
52	12.4	42.7	21	4	US-08-921-944-21	Sequence 37	At
53	12.4	42.7	21	4	US-08-921-944-21	Sequence 38	At
54	12.4	42.7	21	4	US-08-921-944-21	Sequence 39	At
55	12.4	42.7	21	4	US-08-921-944-21	Sequence 40	At
56	12.4	42.7	21	4	US-08-921-944-21	Sequence 41	At
57	12.4	42.7	21	4	US-08-921-944-21	Sequence 42	At
58	12.4	42.7	21	4	US-08-921-944-21	Sequence 43	At
59	12.4	42.7	21	4	US-08-921-944-21	Sequence 44	At
60	12.4	42.7	21	4	US-08-921-944-21	Sequence 45	At
61	12.4	42.7	21	4	US-08-921-944-21	Sequence 46	At
62	12.4	42.7	21	4	US-08-921-944-21	Sequence 47	At
63	12.4	42.7	21	4	US-08-921-944-21	Sequence 48	At
64	12.4	42.7	21	4	US-08-921-944-21	Sequence 49	At
65	12.4	42.7	21	4	US-08-921-944-21	Sequence 50	At
66	12.4	42.7	21	4	US-08-921-944-21	Sequence 51	At
67	12.4	42.7	21	4	US-08-921-944-21	Sequence 52	At
68	12.4	42.7	21	4	US-08-921-944-21	Sequence 53	At
69	12.4	42.7	21	4	US-08-921-944-21	Sequence 54	At
70	12.4	42.7	21	4	US-08-921-944-21	Sequence 55	At
71	12.4	42.7	21	4	US-08-921-944-21	Sequence 56	At
72	12.4	42.7	21	4	US-08-921-944-21	Sequence 57	At
73	12.4	42.7	21	4	US-08-921-944-21	Sequence 58	At
74	12.4	42.7	21	4	US-08-921-944-21	Sequence 59	At
75	12.4	42.7	21	4	US-08-921-944-21	Sequence 60	At
76	12.4	42.7	21	4	US-08-921-944-21	Sequence 61	At
77	12.4	42.7	21	4	US-08-921-944-21	Sequence 62	At
78	12.4	42.7	21	4	US-08-921-944-21	Sequence 63	At
79	12.4	42.7	21	4	US-08-921-944-21	Sequence 64	At
80	12.4	42.7	21				



PS Example 1; Page 49; 140pp; Japanese.

XX The present sequence represents a PCR primer used in the isolation of
CC a human haemophilic receptor protein, HP12. HP12 has immunosuppressive
CC and anti-inflammatory activities and can be used for treating for
CC haemophilic factors with the potential for stimulating autoimmune
CC disease, tissue rejection and allergic against C3, C4, C5 and C6.

XX Sequence 27 BP; 8 A; 7 G; 6 C; 6 T; 0 other;

Query Match 44.7%; Score 13.4; DP 23; Length 27;

Best Local Similarity 73.9%; Pred. No. 1.9e+04;

Matches 17; Conservativity 0; Mismatches 6; Indels 0; Gaps 0;

XX 7 GGGGTAAGACAAATTTCTCT 29

XX 26 GCTCCAGTACAAATTTCTACT 4

RESULT 35

AA87828 standard, DNA, 27 BP.

XX AA87828;

XX 11-JUN-2001 (first entry)

XX Human haemophilic receptor protein, HP12, amino acid sequence,

XX Human haemophilic receptor protein, HP12, amino acid sequence,

XX Human haemophilic receptor protein, HP12, amino acid sequence,

XX Human haemophilic receptor protein, HP12, amino acid sequence,

XX Human haemophilic receptor protein, HP12, amino acid sequence,

XX Homo sapiens.

XX K020123556-A1.

XX 05-APR-2001.

XX 27-SEP-2000; 2000MO-EP06654.

XX 27-SEP-1999; 93JP 027359.

XX 05-AUG-2000; 2000JP-0240397.

XX (CHIR) CHIRON CORP. INVT. MEDICINE MEDICINE INC.

XX Mada M. Yaguchi N.

XX WP1; 2001 26/14/97

XX New haemophilic receptor protein, HP12, amino acid sequence, for

XX binding factors for potential treatment of autoimmune diseases, tissue

XX rejection and allergies

XX Example 1; Page 49; 140pp; Japanese.

XX The present sequence represents a PCR primer used in the isolation of

XX a human haemophilic receptor protein, HP12. HP12 has immunosuppressive

XX and anti-inflammatory activities and can be used for treating for

XX haemophilic factors with the potential for stimulating autoimmune

XX disease, tissue rejection and allergic against C3, C4, C5 and C6.

XX Sequence 27 BP; 6 A; 6 C; 7 G; 6 T; 0 other;

Query Match 44.7%; Score 13.4; DP 23; Length 27;

Best Local Similarity 73.9%; Pred. No. 1.9e+04;

Matches 17; Conservativity 0; Mismatches 6; Indels 0; Gaps 0;

XX 7 GGGGTAAGACAAATTTCTCT 29

XX 26 GCTCCAGTACAAATTTCTACT 4

RESULT 36

AA254731/C

XX AA254731 standard, DNA, 29 BP.

XX AA254731;

XX 21-MAR-2000 (first entry)

XX Neisseria species ORF cloning PCR primer #118.

XX Neisseria meningitidis, Neisseria gonorrhoeae, antigen, vaccine,

XX antigenic, diagnostic, immunogenic, infection, meningitis, septicaemia,

XX antibiotic, gene therapy, PCR primer, ss.

XX Synthetic.

XX Neisseria sp.

XX W09957280-A2.

XX 11-NOV-1999.

XX 30-APR-1999; 99MO-US09346.

XX 01-MAY-1998; 98US-028759.

XX 31-JUL-1998; 98US-0094853.

XX 02-SEP-1998; 98US-0098994.

XX 02-SEP-1998; 98US-0098994.

XX 09-OCT-1998; 98US-0103794.

XX 09-OCT-1998; 98US-0103794.

XX 25-FEB-1995; 95C0-0101028.

XX (CHIR) CHIRON CORP.

XX (CHIR) CHIRON CORP.

XX Fraser C, Galeotti C, Grandi G, Hickey E, Marignani V, Mada M,

XX Peterson J, Pizzi M, Rappelli P, Ratti G, Scialino E, Scarsini M,

XX Tettelin H, Venter CC;

XX WP1; 2000 06/15/95.

XX Novel Neisseria meningitidis predicted to be useful antigens for

XX vaccines and diagnostics

XX Example 1; Page 143; 143pp; English.

XX AA254731 to AA254731; AA254731 to AA254731; and AA254731 to AA254731;

XX represent novel Neisseria meningitidis and Neisseria gonorrhoeae

XX and Neisseria meningitidis and Neisseria gonorrhoeae antigens for

XX PCR primers used in the exemplification of the present invention. The

XX primers can be used as vaccines, as diagnostic reagents, and as

XX reagents for detecting the presence of the bacteria in the

XX manufacture of medicaments for treating or preventing infection due to

XX presence of Neisseria meningitidis and Neisseria gonorrhoeae. They may also

XX be used as antigens for antibodies or for vaccines, which may be

XX used as antigens for antibodies or for vaccines, which may be

XX may also be used in gene therapy protocols.

XX Sequence 29 BP; 8 A; 7 G; 7 C; 7 T; 0 other;

Query Match 44.7%; Score 13.4; DP 23; Length 29;

Best Local Similarity 73.9%; Pred. No. 1.9e+04;

Matches 17; Conservativity 0; Mismatches 6; Indels 0; Gaps 0;

XX 3 AA254731 to AA254731 25

XX 23 AA254731 to AA254731 1

RESULT 37

AA67534/C

ID AA228757 standard, DNA, 33 BP.
 XX
 AC AA228757.
 XX
 DT 01-FEB-2000 (first entry)
 XX
 DE Truncated membrane-translocating peptide sequence coding region #8.
 XX
 KW Membrane-translocating peptide sequence; MTS; fusion protein; production;
 KW Schistosoma japonicum; glutathione S transferase; adenovirus; mammal;
 KW p53; immune response; hepatitis B virus; surface antigen; canine; feline;
 KW protease inhibitor; cancer; tumor suppressor; feline; ss
 XX
 OS Synthetic.
 XX
 PN WO9949879 A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US07189.
 XX
 PR 31-MAR-1999; 99US-0060083.
 PR 04-NOV-1999; 99US-0186170.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Lin Y, Donahue JP, Rojas M, Tan ZJ.
 XX
 DR WPI: 1999.610819/52.
 DR P-PSUR: AAY44160.
 XX
 PT New peptides containing a membrane-translocating sequence used to
 PT develop products for use in, e.g. vaccines.
 XX
 PS Disclosure, Page 9, 85pp; English.
 XX
 CC Sequence AA228757 correct reference truncated coding regions based on
 CC the coding region of a novel membrane-translocating peptide sequence
 CC (MTS, AA228749). The invention relates to the use of the MTS peptides
 CC for generating fusion proteins which can be used for the production of
 CC polypeptides of interest such as a viral protein, glutathione
 CC transferase, an adenovirus E3 19K protein or a mammalian p53 protein.
 CC Fusions of the peptides can also be used for inducing an immune response
 CC in a mammal using a viral polypeptide such as hepatitis B
 CC surface antigen. They can also be used for protecting a subject from an
 CC infectious agent using a polypeptide that inhibits reproduction of the
 CC infectious agent such as a protease inhibitor. They can also be used for
 CC treating a subject using a polypeptide that suppresses such as p53 protein
 CC or a polypeptide inhibitor of p53. The methods can be used for
 CC treating canine, feline and bovine diseases and also for studying
 CC intracellular proteins.
 XX
 SQ Sequence 33 BP, 1 A, 15 C, 5 G, 12 T, 0 other;
 XX
 QW Query Match 46.7%, Score 14, DB 20, Length 33,
 Best Local Similarity 100.0%, Pred No. Ident 14,
 Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
 XX
 QY 6 TGGCGACAGAGAA 19
 |||||
 DB 30 TGGCGACAGAGAA 17
 XX
 RESULT 24
 AA228749
 ID AA228749 standard, DNA, 34 BP.
 XX
 AC AA228749.
 XX
 DT 01-FEB-2000 (first entry)
 XX
 DE Membrane-translocating peptide sequence coding region.
 XX

KW Membrane-translocating peptide sequence; MTS; fusion protein; production;
 KW Schistosoma japonicum; glutathione S transferase; adenovirus; mammal;
 KW p53; immune response; hepatitis B virus; surface antigen; canine; feline;
 KW protease inhibitor; cancer; tumor suppressor; feline; ss
 XX
 OS Synthetic.
 XX
 PN WO9949879 A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US07189.
 XX
 PR 31-MAR-1999; 99US-0060083.
 PR 04-NOV-1999; 99US-0186170.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Lin Y, Donahue JP, Rojas M, Tan ZJ.
 XX
 DR WPI: 1999.610819/52.
 DR P-PSUR: AAY44160.
 XX
 PT New peptides containing a membrane-translocating sequence used to
 PT develop products for use in, e.g. vaccines.
 XX
 PS Disclosure, Page 8, 85pp; English.
 XX
 CC This sequence represents the coding region for a novel membrane-
 CC translocating peptide sequence (MTS). The invention relates to the use
 CC of the MTS peptides for generating fusion proteins which can be used for
 CC the production of polypeptides of interest such as a viral protein, glutathione
 CC transferase, an adenovirus E3 19K protein or a mammalian p53 protein.
 CC Fusions of the peptides can also be used for inducing an
 CC immune response in a mammal using e.g. a viral polypeptide such as
 CC hepatitis B surface antigen. They can also be used for protecting a
 CC subject from an infectious agent using a polypeptide that inhibits
 CC reproduction of the infectious agent such as a protease inhibitor.
 CC They can also be used for treating cancer using a polypeptide that
 CC suppresses such as p53 protein or a polypeptide inhibitor of p53.
 CC The methods can be used for treating canine, feline and bovine diseases
 CC and also for studying intracellular proteins.
 XX
 SQ Sequence 34 BP, 2 A, 14 C, 6 G, 12 T, 0 other;
 XX
 QW Query Match 46.7%, Score 14, DB 20, Length 34,
 Best Local Similarity 100.0%, Pred No. Ident 14,
 Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
 XX
 QY 6 TGGCGACAGAGAA 19
 |||||
 DB 33 TGGCGACAGAGAA 20
 XX
 RESULT 25
 AA228749
 ID AA228749 standard, DNA, 34 BP.
 XX
 AC AA228749.
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE PCR primer used to amplify an CPE of Chlamydia pneumoniae.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; streptococcus;
 KW sinusitis; paratubercular infection; systemic infection; pharyngitis;
 KW vaccine; neutralizing epitope; PCR primer; ss.
 XX
 OS Synthetic.
 OS Chlamydia pneumoniae.
 XX
 FN WC9927105 A2.
 XX

PT Lin Y, Donahue JP, Rojas M, Tan ZJ;
 XX
 TF WPI, 1999-610919/52.
 DR P-PSDB; AA44165.
 XX
 XX
 PT New peptides containing a membrane translocating sequence used to
 IT develop products for use in, e.g., vaccines.
 XX
 PS Disclosure, Page 3; 85pp; English.
 XX
 CC Sequences AAC28755, 229977 represent truncated coding regions based on
 CC the coding region of a novel membrane-translocating peptide sequence
 CC (MTR; AAC28755). The invention relates to the use of the MTR peptides
 CC for generating fusion proteins which can be used for the production of
 CC polypeptides of interest such as Schistosoma japonicum glutathione S
 CC transferase, an adenovirus E1 19k protein or a mammalian p53 protein.
 CC Fusions of the peptides can also be used for inducing an immune response
 CC in a mammal using e.g. a viral polypeptide such as hepatitis B
 CC surface antigen. They can also be used for detecting a subject from an
 CC infectious agent using a polypeptide that inhibits reproduction of the
 CC infectious agent such as a protease inhibitor. They can also be used for
 CC treating cancer using a polypeptide-tumor suppressor such as p53 protein
 CC or a cell cycle inhibitor. The peptides can be used for
 CC treating cancer, killing and lysing tumours, leprosy and AIDS for studying
 CC intracellular proteins.
 XX
 SO Sequence 24 BP; 1 A; 12 C; 4 G; 8 T; 0 Other;
 Query Match: 46 78, Score 14; DR 24; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9,88+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0Y 6 TGGCGACAGAGAA 19
 21 TGGCGACAGAGAA 8
 2b
 RESULT 19
 ARL61515
 ID ARL61515 standard; DNA; 24 BP.
 XX
 AC ARL61515;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human cell cycle inhibitor 11-66 H125 Filippi 201 10 4
 XX
 KW Fudopolyepitide 11 66 malignant tumour; haematology; HIV infection;
 KW human immune deficiency virus; immunological disorder; inflammation;
 KW human; PCR; primers; ss.
 XX
 OS Homo sapiens.
 XX
 PR CNI31746 A.
 XX
 PD 27 MAR 2002.
 XX
 PF 07 SEP 2000; 2000CN-0125087.
 XX
 PR 07 SEP 2000; 2000CN-0125087.
 XX
 PA (SWAN) SWANMAN; RI 0006; SEPR; SVV; 00 110;
 XX
 PI Mao Y, Xin Y.
 XX
 DR WPI; 2002-509473/55
 XX
 PT New polypeptide human cell cycle inhibitor 11 66 for treating malignant
 PT tumor, hematology, human immunodeficiency virus infection, immunology and
 PT disease and various inflammations
 XX
 PR Example 1, Page 17, 18pp; Chinese

CC This invention describes a novel human anti-polyepitide 11 66, the
 CC polypeptide encoding the polypeptide and a method of producing the
 CC polypeptide by using DNA recombinant technology. The invention also
 CC discloses curing several diseases, such as malignant tumors, hematology,
 CC human immunodeficiency virus (HIV) infection, immunological disorder and
 CC various inflammations using the polypeptide. The invention also discloses
 CC an antagonist for treating the polypeptide and its treatment in animal.
 CC This sequence represents a RT-PCR primer used in the amplification of the
 CC human anti-polyepitide 11 66 gene described in the disclosure of the
 CC invention.
 XX
 SO Sequence 24 BP; 8 A; 3 C; 4 G; 8 T; 1 Other;
 Query Match: 46 78, Score 14; DR 24; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9,88+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0Y 4 ATTGGACAGAGAAATTTT 25
 3 ATTGGACAGAGAGAAATTTT 24
 2b
 RESULT 20
 AAC28755/C
 ID AAC28755 standard; DNA; 26 BP.
 XX
 AC AAC28755;
 XX
 DT 01 FEB 2002 (first entry)
 XX
 DE Truncated membrane-translocating peptide sequence used in region 16.
 XX
 KW Membrane-translocating peptide sequence; MTR; fusion protein; production;
 KW Schistosoma japonicum; glutathione S transferase; adenovirus; mammalian
 KW p53; immune response; hepatitis B virus; surface antigen; cancer; tumor;
 KW protease inhibitor; cancer; tumor suppressor; protein; ss.
 XX
 OS Synthetic.
 XX
 PR WO9949879-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 41-MAP-1999; 99WO-0807189.
 XX
 PR 41-MAP-1999; 99WO-0807189;
 XX
 PR 04-NOV-1998; 98US-0196170;
 XX
 PA (TIVA) UNIV VANDERBILT.
 XX
 PI Lin Y, Donahue JP, Rojas M, Tan ZJ;
 XX
 DR WPI; 1999-610919/52.
 XX
 DR P-PSDB; AA44165.
 XX
 PT New peptides containing a membrane translocating sequence used to
 IT develop products for use in, e.g., vaccines
 XX
 PS Disclosure, Page 3; 85pp; English.
 XX
 CC Sequences AAC28755, 229977 represent truncated coding regions based on
 CC the coding region of a novel membrane translocating peptide sequence
 CC (MTR; AAC28755). The invention relates to the use of the MTR peptides
 CC for generating fusion proteins which can be used for the production of
 CC polypeptides of interest such as Schistosoma japonicum glutathione S
 CC transferase, an adenovirus E1 19k protein or a mammalian p53 protein.
 CC Fusions of the peptides can also be used for detecting an infectious
 CC surface antigen. They can also be used for detecting a subject from an
 CC infectious agent using a polypeptide that inhibits reproduction of the
 CC infectious agent such as a protease inhibitor. They can also be used for
 CC treating cancer using a polypeptide-tumor suppressor such as p53 protein
 CC or a polypeptide inhibitor of Bcl-2. The methods can be used for

CC phenotypic. The reference RNA transcript would bind to native mRNA and
 CC interfere with translation.

XX Sequence 27 BP; 4 A; 8 C; 6 G; 9 T; 0 other;

Query Match 47 34, Score 14.2, LE 11, Length 27,
 Best Local Similarity 84.28; Pred. No. 8,10,03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATATTTTCTTATATATATA 19
 DB 20 GCAATTCGCGACAGAGTA 2

RESULT 14

ABL99409/C
 ID ABL99409 standard, DNA, 27 BP

XX ABL99409;

AC 02-JUL-2002 (first entry)

XX Right PCR primer used to target ubiquitin canine gene.

XX Canine gene array, 1000-bp (1000-bp) ss.

XX Canis sp.

XX WO200208451-A2.

XX 31 JAN 2002.

XX 23-JUL-2002; 2001WD US23511.

XX 21-JUL-2002; 2000US-220057P.

XX (PHEAS-1) MOLECULAR TOXICOLOGY.

XX Fast SP, Picked 93, Nette PE, Dunn RT.

XX WPI; 2002-01-01/02/03.

XX Identifying a specific canine gene to determine

XX local array of responses of approximately 2000 genes

XX expression profiles of untreated canine cells and canine cells treated

XX with an agent.

XX Example: Fig. 1, 14BP, English.

XX This invention relates to identifying a toxicologically relevant canine

XX gene and the generation of an array of 1000-10000 genes.

XX canine gene. The gene array is useful for obtaining a gene expression

XX profile, by comparing a particular set of cells with a set of cells

XX from the population of cells, including the cDNA, and extracting the cDNA

XX arrays to determine toxicological responses to various agents, and also

XX the method for analyzing toxicological responses and level canine genes.

XX The method for analyzing toxicological responses using the canine

XX gene array is rapid and efficient. The present sequence is related

XX to the canine gene array.

RESULT 15

AAFP0805
 ID AAFP0805 standard, DNA, 30 BP.

XX AAFP0805;

XX 21 JUN 2001 (first entry)

XX Hydnatoxin racemase gene PCR primer S1138.

XX Hydnatoxin racemase, hydn gene, amino acid (hydroxy acid) PCR primer

XX ss.

XX Archaeobacter aureusens.

XX WO200123525 A2.

XX 05 APR 2001.

XX 02-SEP-2000; 2000WD-EP08580.

XX 27-SEP-1999; 1999P-0119956.

XX (DECS) DEUSSA-HUBIS AG.

XX (UYST-) UNIV STUTTGART.

XX (HOF) FACHFACHSTREITEN GMBH.

XX Altenbucher J, Matthes R, Pietzsch M, Sydansk C, Wiese A;

XX Bommaritus A, Tischer W;

XX WPI; 2001-281641/29.

XX Novel rec-Hydnatoxin-racemase from Archaeobacter aureusens DSM 1747

XX (hydn) useful for producing enantiomerically enriched amino acids

XX acids or its derivatives on industrial scale

XX Example; Page 8; 21BP; English.

XX The present sequence is that of primer S1138, designed for the

XX PCR amplification of the hydnatoxin racemase gene (hydn), see

XX AAFP0806 of Archaeobacter aureusens DSM 1747. S1138 was used with

XX primer S1137 (see AAFP0804) for the PCR, with pMT as template.

XX The PCR product was inserted into expression vector pR2702,

XX creating E. coli strain S1138, which was utilized for the production of

XX recombinant hydnatoxin racemase in Escherichia coli JM109

XX transformants. A library for the gene encoding the hydnatoxin

XX racemase is claimed. The recombinant enzyme is able to racemize

XX hydnatoxin and other hydroxy acids with a rate acceptable

XX for implementation in an industrial scale. The use of the

XX racemase in processes for the production of amino acid hydroxy acids

XX or their derivatives, and of enantiomerically enriched compounds,

XX concluded in an enzyme-mediated process is also claimed.

XX Sequence 30 BP; 4 A; 7 C; 7 G; 8 T; 6 other;

XX Query Match 47 34, Score 14.2, DP 22, Length 30,
 Best Local Similarity 70.48; Pred. No. 8, 20, 03;
 Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 AATTCGCGCGACAGAGTA 23
 DB 3 AACTGCGCGCGACAGAGTA 29

RESULT 16
 AAF08548/C
 ID AAF08548 standard, DNA, 30 BP.
 XX AAF08548;
 XX 14-JUL-2002 (first entry)
 XX Parathyroid hormone receptor reverse transcriptase PCR primer #1.
 XX

P1 Becker DL, Green CR;
 XX
 DR WPI; 2000-491220/43
 XX
 PT New formulation for therapeutic and/or cosmetic treatment of neuronal
 PT cell death, inflammation and scar formation, comprising antisense
 PT polynucleotide to connexin protein
 XX
 PS Claim 9; Page 2; 64pp; English
 XX
 CC This invention describes a novel formulation (I) for use in therapeutic
 CC and/or cosmetic treatment, comprising at least one antisense
 CC polynucleotide (II) to a connexin protein together with a carrier
 CC vehicle. The formulation of the invention has been found to be useful in a
 CC formulation (II) which is administered to a site on or within a patient
 CC for the site-specific downregulation of connexin protein expression. (I)
 CC is therefore specifically useful for reducing neuronal cell death
 CC resulting from neuronal trauma, a physical trauma to the brain, spinal
 CC cord or other parts of a patient, for preventing wound healing resulting
 CC from trauma, burns or surgery and for reducing inflammation as a result
 CC of a wound or physical trauma to the brain, spinal cord or other parts
 CC and for decreasing scar formation. (I) containing (II) directed to
 CC connexin 43 or 32 is administered to regulate epithelial (E) at (I)
 CC downregulation and growth of a wound or a physical trauma to the brain,
 CC respectively, for skin regeneration or thickening for cosmetic or
 CC therapeutic purposes (I) containing (II) containing (II) directed to
 CC connexin 43 or 32 is administered to regulate epithelial (E) at (I)
 CC directed oligonucleotide which is used in the method of the invention.
 XX
 CC Sequence 30 BP; 6 A; 4 G; 10 G; 10 T; 0 other
 XX
 Query March 89.38; Score 26.9; DB 21; Length 30;
 Best Local Similarity 23.28; Pred. No. 0.024;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 1 GGAATTCGGGCAAGACAAATGTTTCGTC 30
 1 GGAATTCGGGCAAGACAAATGTTTCGTC 30
 1 GGAATTCGGGCAAGACAAATGTTTCGTC 30
 XX
 RESULT 3
 AAA71652/c
 ID AAA71652 standard; DNA; 30 BP.
 AC
 AA71652;
 XX
 CT 15-DEC-2000 (first entry)
 XX
 DE Connexin 43 primer sequence DNA
 XX
 KW Connexin 43 is a protein that is involved in the regulation of
 KW intercellular communication, particularly in the brain, spinal cord and
 KW peripheral innervation. Brain/spinal cord/spinal nerve wound healing
 KW inflammation reduction, scar formation, epithelial (E) at (I) downregulation,
 KW regeneration, skin regeneration, primer, chicken, ss.
 XX
 OS Unidentified.
 XX
 PN W0200044409-A1.
 XX
 PD 01-AUG-2000.
 XX
 EF 27-JAN-2000; 2000W-080038.
 XX
 FR 27-JAN-1999; 99NZ-0333928.
 FR 07-OCT-1999; 99NZ-0500190.
 XX
 IN UNO; UNIV COLLEGE LONDON.
 XX
 PI Becker DL, Green CR;
 XX
 DR WPI; 2000-491220/43

XX
 PT New formulation for therapeutic and/or cosmetic treatment of neuronal
 PT cell death, inflammation and scar formation, comprising antisense
 PT polynucleotide to connexin protein
 XX
 PS Example 1; Page 17; 64pp; English.
 XX
 CC This invention describes a novel formulation (I) for use in therapeutic
 CC and/or cosmetic treatment, comprising at least one antisense
 CC polynucleotide (II) to a connexin protein together with a carrier
 CC vehicle. The formulation of the invention has been found to be useful in a
 CC formulation (II) which is administered to a site on or within a patient
 CC for the site-specific downregulation of connexin protein expression. (I)
 CC is therefore specifically useful for reducing neuronal cell death
 CC resulting from neuronal trauma, a physical trauma to the brain, spinal
 CC cord or other parts of a patient, for preventing wound healing resulting
 CC from trauma, burns or surgery and for reducing inflammation as a result
 CC of a wound or physical trauma to the brain, spinal cord or other parts
 CC and for decreasing scar formation. (I) containing (II) directed to
 CC connexin 43 or 32 is administered to regulate epithelial (E) at (I)
 CC downregulation and growth of a wound or a physical trauma to the brain,
 CC respectively, for skin regeneration or thickening for cosmetic or
 CC therapeutic purposes (I) containing (II) containing (II) directed to
 CC connexin 43 or 32 is administered to regulate epithelial (E) at (I)
 CC directed oligonucleotide which is used in the method of the invention.
 XX
 CC Sequence 30 BP; 13 A; 13 G; 4 T; 0 other
 XX
 Query March 89.38; Score 26.8; DB 21; Length 30;
 Best Local Similarity 23.28; Pred. No. 0.024;
 Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 1 GGAATTCGGGCAAGACAAATGTTTCGTC 30
 30 GGAATTCGGGCAAGACAAATGTTTCGTC 1
 30 GGAATTCGGGCAAGACAAATGTTTCGTC 1
 XX
 RESULT 4
 AAA71653
 ID AAA71653 standard; DNA; 30 BP.
 AC
 AA71653;
 XX
 DT 15-DEC-2000 (first entry)
 XX
 DE Chicken connexin 43 primer DB1 DNA.
 XX
 KW Connexin 43 is a protein that is involved in the regulation of
 KW intercellular communication, particularly in the brain, spinal cord and
 KW peripheral innervation. Brain/spinal cord/spinal nerve wound healing
 KW inflammation reduction, scar formation, epithelial (E) at (I) downregulation,
 KW regeneration, skin regeneration, primer, chicken, ss.
 XX
 OS Gallus sp.
 XX
 PN W0200044409-A1.
 XX
 PD 03-AUG-2000.
 XX
 EF 27-JAN-2000; 2000W-080038.
 XX
 FR 27-JAN-1999; 99NZ-0333928.
 FR 07-OCT-1999; 99NZ-0500190.
 XX
 IN UNO; UNIV COLLEGE LONDON.
 XX
 PI Becker DL, Green CR;
 XX
 DR WPI; 2000-491220/43.
 XX
 PT New formulation for therapeutic and/or cosmetic treatment of neuronal
 PT cell death, inflammation and scar formation, comprising antisense

C 175	11.4	38.0	13	23	ABG61860	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103512	Cytosine deaminase
C 176	11.4	38.0	13	23	ABG61861	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103513	Glutamate decarboxylase
C 177	11.4	38.0	13	23	ABG76860	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103514	Glutamate decarboxylase
C 378	11.4	38.0	13	23	ABG76861	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103515	Glutamate decarboxylase
C 379	11.4	38.0	13	23	ABG76862	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103516	Glutamate decarboxylase
C 380	11.4	38.0	13	23	ABG76863	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103517	Glutamate decarboxylase
C 381	11.4	38.0	13	23	ABG76864	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103518	Glutamate decarboxylase
C 382	11.4	38.0	13	23	ABG76865	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103519	Glutamate decarboxylase
C 383	11.4	38.0	13	23	ABG76866	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103520	Glutamate decarboxylase
C 384	11.4	38.0	13	23	ABG76867	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103521	Glutamate decarboxylase
C 385	11.4	38.0	13	23	ABG76868	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103522	Glutamate decarboxylase
C 386	11.4	38.0	13	23	ABG76869	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103523	Glutamate decarboxylase
C 387	11.4	38.0	13	23	ABG76870	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103524	Glutamate decarboxylase
C 388	11.4	38.0	13	23	ABG76871	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103525	Glutamate decarboxylase
C 389	11.4	38.0	13	23	ABG76872	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103526	Glutamate decarboxylase
C 390	11.4	38.0	13	23	ABG76873	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103527	Glutamate decarboxylase
C 391	11.4	38.0	13	23	ABG76874	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103528	Glutamate decarboxylase
C 392	11.4	38.0	13	23	ABG76875	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103529	Glutamate decarboxylase
C 393	11.4	38.0	13	23	ABG76876	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103530	Glutamate decarboxylase
C 394	11.4	38.0	13	23	ABG76877	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103531	Glutamate decarboxylase
C 395	11.4	38.0	13	23	ABG76878	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103532	Glutamate decarboxylase
C 396	11.4	38.0	13	23	ABG76879	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103533	Glutamate decarboxylase
C 397	11.4	38.0	13	23	ABG76880	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103534	Glutamate decarboxylase
C 398	11.4	38.0	13	23	ABG76881	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103535	Glutamate decarboxylase
C 399	11.4	38.0	13	23	ABG76882	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103536	Glutamate decarboxylase
C 400	11.4	38.0	13	23	ABG76883	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103537	Glutamate decarboxylase
C 401	11.4	38.0	13	23	ABG76884	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103538	Glutamate decarboxylase
C 402	11.4	38.0	13	23	ABG76885	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103539	Glutamate decarboxylase
C 403	11.4	38.0	13	23	ABG76886	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103540	Glutamate decarboxylase
C 404	11.4	38.0	13	23	ABG76887	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103541	Glutamate decarboxylase
C 405	11.4	38.0	13	23	ABG76888	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103542	Glutamate decarboxylase
C 406	11.4	38.0	13	23	ABG76889	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103543	Glutamate decarboxylase
C 407	11.4	38.0	13	23	ABG76890	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103544	Glutamate decarboxylase
C 408	11.4	38.0	13	23	ABG76891	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103545	Glutamate decarboxylase
C 409	11.4	38.0	13	23	ABG76892	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103546	Glutamate decarboxylase
C 410	11.4	38.0	13	23	ABG76893	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103547	Glutamate decarboxylase
C 411	11.4	38.0	13	23	ABG76894	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103548	Glutamate decarboxylase
C 412	11.4	38.0	13	23	ABG76895	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103549	Glutamate decarboxylase
C 413	11.4	38.0	13	23	ABG76896	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103550	Glutamate decarboxylase
C 414	11.4	38.0	13	23	ABG76897	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103551	Glutamate decarboxylase
C 415	11.4	38.0	13	23	ABG76898	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103552	Glutamate decarboxylase
C 416	11.4	38.0	13	23	ABG76899	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103553	Glutamate decarboxylase
C 417	11.4	38.0	13	23	ABG76900	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103554	Glutamate decarboxylase
C 418	11.4	38.0	13	23	ABG76901	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103555	Glutamate decarboxylase
C 419	11.4	38.0	13	23	ABG76902	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103556	Glutamate decarboxylase
C 420	11.4	38.0	13	23	ABG76903	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103557	Glutamate decarboxylase
C 421	11.4	38.0	13	23	ABG76904	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103558	Glutamate decarboxylase
C 422	11.4	38.0	13	23	ABG76905	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103559	Glutamate decarboxylase
C 423	11.4	38.0	13	23	ABG76906	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103560	Glutamate decarboxylase
C 424	11.4	38.0	13	23	ABG76907	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103561	Glutamate decarboxylase
C 425	11.4	38.0	13	23	ABG76908	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103562	Glutamate decarboxylase
C 426	11.4	38.0	13	23	ABG76909	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103563	Glutamate decarboxylase
C 427	11.4	38.0	13	23	ABG76910	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103564	Glutamate decarboxylase
C 428	11.4	38.0	13	23	ABG76911	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103565	Glutamate decarboxylase
C 429	11.4	38.0	13	23	ABG76912	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103566	Glutamate decarboxylase
C 430	11.4	38.0	13	23	ABG76913	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103567	Glutamate decarboxylase
C 431	11.4	38.0	13	23	ABG76914	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103568	Glutamate decarboxylase
C 432	11.4	38.0	13	23	ABG76915	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103569	Glutamate decarboxylase
C 433	11.4	38.0	13	23	ABG76916	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103570	Glutamate decarboxylase
C 434	11.4	38.0	13	23	ABG76917	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103571	Glutamate decarboxylase
C 435	11.4	38.0	13	23	ABG76918	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103572	Glutamate decarboxylase
C 436	11.4	38.0	13	23	ABG76919	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103573	Glutamate decarboxylase
C 437	11.4	38.0	13	23	ABG76920	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103574	Glutamate decarboxylase
C 438	11.4	38.0	13	23	ABG76921	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103575	Glutamate decarboxylase
C 439	11.4	38.0	13	23	ABG76922	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103576	Glutamate decarboxylase
C 440	11.4	38.0	13	23	ABG76923	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103577	Glutamate decarboxylase
C 441	11.4	38.0	13	23	ABG76924	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103578	Glutamate decarboxylase
C 442	11.4	38.0	13	23	ABG76925	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103579	Glutamate decarboxylase
C 443	11.4	38.0	13	23	ABG76926	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103580	Glutamate decarboxylase
C 444	11.4	38.0	13	23	ABG76927	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103581	Glutamate decarboxylase
C 445	11.4	38.0	13	23	ABG76928	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103582	Glutamate decarboxylase
C 446	11.4	38.0	13	23	ABG76929	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103583	Glutamate decarboxylase
C 447	11.4	38.0	13	23	ABG76930	oligonucleotide SE	C 440	11.4	48.0	30	16	AA103584	Glutamate decarboxylase



```

source 1.21
/organism="unknown"
BASE COUNT 4 a 4 c 5 g 8 t
ORIGIN
Query Match 42.7% Score 12.8, FR 6, Length 21;
Best Local Similarity 97.5% Pred. No. 4, 9e+05;
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 11 CAGAGAGATTGTTC 26
|||||
20 CAGAGAGATTGTTC 5

RESULT 37
LOCUS AR122836 23 bp DNA linear PAT 16 MAY 2001
DEFINITION Escherichia coli strain ATCC 8739.
ACCESSION AR122836
VERSION AR122836.1 GI:14107802
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 23)
AUTHORS
Jung, J. N., Gold, L., Schmidt, P., and Vignuzzi, T.
TITLE
Vaccinia (orthopoxvirus) growth factor (VGF) Nucleic Acid Ligand
Complexes
JOURNAL
Patent: US 6169779 A 59 02 JAN 2001;
FEATURES
Location/Qualifiers
source
BASE COUNT 7 a 3 c 10 g 3 t
ORIGIN
Query Match 42.7% Score 12.8, FR 6, Length 21;
Best Local Similarity 97.5% Pred. No. 4, 9e+05;
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 7 GCGGCAAGAGAGATTG 22
|||||
1 GCGGTAGGAGAGATTG 16

RESULT 38
LOCUS AR122862 24 bp DNA linear PAT 16 MAY 2001
DEFINITION Escherichia coli strain ATCC 8739.
ACCESSION AR122862
VERSION AR122862.1 GI:14107923
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 24)
AUTHORS
Jung, J. N., Gold, L., Schmidt, P., and Vignuzzi, T.
TITLE
Vaccinia (orthopoxvirus) growth factor (VGF) Nucleic Acid Ligand
Complexes
JOURNAL
Patent: US 6168778-A 84 02 JAN 2001;
FEATURES
Location/Qualifiers
source
BASE COUNT 7 a 3 c 10 g 3 t
ORIGIN
Query Match 42.7% Score 12.8, FR 6, Length 23;
Best Local Similarity 97.5% Pred. No. 4, 9e+05;
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 7 GCGGCAAGAGAGATTG 22
|||||
1 GCGGTAGGAGAGATTG 16

```

```

RESULT 39
LOCUS IS7019 24 bp DNA linear PAT 06 SEP 1997
DEFINITION Sequence 19 from patent US 5650553.
ACCESSION IS7019
VERSION IS7019.1 GI:1270432
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 24)
AUTHORS
Ecker, J., Rothenberg, M., Lehman, A., and Roman, G.
TITLE
Plant genes for sensitivity to ethylene and pathogenesis
JOURNAL
Patent: US 5650553-A 15 02 JUL 1997;
FEATURES
Location/Qualifiers
source
BASE COUNT 7 a 5 c 4 g 8 t
ORIGIN
Query Match 42.7% Score 12.8, FR 6, Length 23;
Best Local Similarity 97.5% Pred. No. 4, 9e+05;
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 6 TGGGCAAGAGAGATTGTTC 29
|||||
1 TGGGTAGGAGAGATTGTTC 24

RESULT 40
LOCUS AX214402 29 bp DNA linear PAT 06 SEP 2001
DEFINITION Sequence 10 from Patent WO0159450.
ACCESSION AX214402
VERSION AX214402.1 GI:15521476
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 29)
AUTHORS
Case, C.
TITLE
Cells for drug discovery
JOURNAL
Patent: WO 0159450-A 10 16 AUG 2001;
Sangamo Biosciences Inc. (US)
FEATURES
Location/Qualifiers
source
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer SP67"
BASE COUNT 12 a 6 c 9 g 2 t
ORIGIN
Query Match 42.7% Score 12.8, FR 6, Length 23;
Best Local Similarity 97.5% Pred. No. 4, 9e+05;
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 4 ATTGGGCAAGAGAGAA 19
|||||
7 ATTTCGGCAAGAGAA 22

```

Search completed: July 23, 2003, 14:34:39
 Job time : 329.497 secs

Matches 16; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAATGAGGAAAGAAATTTT 24

Db 9 TAAATGAGGAAAGAAATTTT 31

RESULT 32
Accession: A62700.1 GI:6732429

DEFINITION: Sequence 46 from Patent WO9606646

ACCESSION: A62700.1 GI:6732429

KEYWORDS: Chlamydia psittaci

SOURCE: Chlamydia psittaci

ORGANISM: Chlamydia psittaci

REFERENCE: 1 (bases 1 to 32)

AUTHORS: Ludwig, M. and Schaefer, K.

TITLE: 20S RIBOSOMAL RIBOPROTEIN OF THE CHLAMYDIA GENUS BACTERIA, USES

IN PCR, RT-PCR, AND IN A FRAGMENT AND A DETECTION AND A DETECTION

METHOD: Patent: WO 9606646-A 45 10-DEC-1996

FEATURES: LOCATION/Qualifiers

BASE COUNT: 10 a 8 c 6 g 8 t

ORIGIN: /db_xref="taxon:83554"

Query Match: 43.3% Score 13; DB 6; Length 32;

Best Local Similarity: 76.2% Pred. No. 4e+05;

Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 TAAATGAGGAAAGAAATTTT 22

Db 1 TAAATGAGGAAAGAAATTTT 21

RESULT 33
Accession: A43091.1 GI:2298466

DEFINITION: Sequence 21 from Patent WO9604754.

ACCESSION: A43091.1 GI:2298466

KEYWORDS: unclassified.

SOURCE: unclassified.

ORGANISM: unclassified.

REFERENCE: 1 (bases 1 to 35)

AUTHORS: Probst, M. F., Cammue, B. P. and Povey, S. P.

TITLE: ANTIMICROBIAL PROTEINS

JOURNAL: Patent: WO 9504754-A 21 10-FEB-1995

COMMENT: ZENRCA LTD (GB)

FEATURES: Other publication: CA 416430 300316

BASE COUNT: 10 a 8 c 6 g 8 t

ORIGIN: /db_xref="taxon:83554"

Query Match: 43.3% Score 13; DB 6; Length 35;

Best Local Similarity: 76.2% Pred. No. 4e+05;

Matches 16; Conservative 0; Mismatches 5; Indels 0;

RESULT 34
Accession: AP014670.1 GI:1972124

DEFINITION: Sequence 21 from Patent US 5707645.

ACCESSION: AP014670.1 GI:1972124

KEYWORDS: unclassified.

SOURCE: unclassified.

ORGANISM: unclassified.

REFERENCE: 1 (bases 1 to 35)

AUTHORS: Probst, M. F., Cammue, B. P., and Povey, S. P.

TITLE: ANTIMICROBIAL PROTEINS

JOURNAL: Patent: US 5707645-A 21 10-JUN-1998

FEATURES: LOCATION/Qualifiers

BASE COUNT: 9 a 8 c 10 g 8 t

ORIGIN: /db_xref="taxon:83554"

Query Match: 43.3% Score 13; DB 6; Length 35;

Best Local Similarity: 76.2% Pred. No. 4e+05;

Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 TAAATGAGGAAAGAAATTTT 21

Db 1 TAAATGAGGAAAGAAATTTT 11

RESULT 35
Accession: AP098875.1 GI:12808641

DEFINITION: Sequence 10 from Patent US 5707645.

ACCESSION: AP098875.1 GI:12808641

KEYWORDS: unclassified.

SOURCE: unclassified.

ORGANISM: unclassified.

REFERENCE: 1 (bases 1 to 21)

AUTHORS: Trofatter, J. A., MacCollin, M. M. and Gusev, I. A.

TITLE: Tumor suppressor protein and antibodies thereof

JOURNAL: Patent: US 5707645-A 21 10-JUN-1998

FEATURES: LOCATION/Qualifiers

BASE COUNT: 4 a 4 c 5 g 8 t

ORIGIN: /db_xref="taxon:83554"

Query Match: 42.7% Score 12.8; DB 6; Length 21;

Best Local Similarity: 87.5% Pred. No. 4.7e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 TAAATGAGGAAAGAAATTTT 26

Db 1 TAAATGAGGAAAGAAATTTT 5

RESULT 36
Accession: T79715.1 GI:1298005

DEFINITION: Sequence 10 from Patent US 5707643.

ACCESSION: T79715.1 GI:1298005

KEYWORDS: unclassified.

SOURCE: unclassified.

ORGANISM: unclassified.

REFERENCE: 1 (bases 1 to 21)

AUTHORS: Trofatter, J. A., MacCollin, M. M. and Gusev, I. A.

TITLE: Tumor suppressor gene protein

JOURNAL: Patent: US 5707643-A 21 10-JUN-1998

FEATURES: LOCATION/Qualifiers

COMMENT: Patent: WO 0204522-A 23-17-02M-0002;
 The Scripps Research Institute (US)
 FEATURES
 SOURCE
 1..35
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="FOR SEQUENCING: primer for subcloning FAV-1 19th chain
 for whole antibody by PCR amplification."
 BASE COUNT 11 a 11 c 7 g 6 t
 ORIGIN
 Query Match 44 83; Score 12.0; E=5; Length 35;
 Best local similarity 22.0; First No. 100000
 Matches 15; Conservation 0; Mismatches 3; Indels 0; Gaps 0
 CY 13 AGAAGATTGTTCTTC 30
 DB 35 AGCAGATTGTTCTTC 19
 RESULT 28
 AR094621/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Unclassified.
 REFERENCE
 1 (bases 1 to 23)
 Bergsma, D.J. and Tanigawa, M.
 Ligands of the hepatotropic protein HPGAN2
 Patent: US 6001674 A 14-07-1999.
 FEATURES
 SOURCE
 1..23
 /organism="unknown"
 BASE COUNT 4 a 7 c 9 g 4 t
 ORIGIN
 Query Match 43 74; Score 13; E=6; Length 23;
 Best local similarity 26.0; First No. 100000
 Matches 15; Conservation 0; Mismatches 5; Indels 0; Gaps 0
 CY 10 GCGAGAGAGATTGTTCTTC 30
 DB 22 GCGAGAGAGATTGTTCTTC 2
 RESULT 29
 AR175701/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown
 Unclassified.
 REFERENCE
 1 (bases 1 to 23)
 Bergsma, D.J. and Tanigawa, M.
 Ligands of the hepatotropic protein HPGAN2
 Patent: US 6001674 A 14-07-1999.
 FEATURES
 SOURCE
 1..23
 /organism="unknown"
 BASE COUNT 4 a 7 c 9 g 4 t
 ORIGIN
 Query Match 43 74; Score 13; E=6; Length 23;
 Best local similarity 26.0; First No. 100000
 Matches 15; Conservation 0; Mismatches 5; Indels 0; Gaps 0
 CY 10 GCGAGAGAGATTGTTCTTC 30
 DB 22 GCGAGAGAGATTGTTCTTC 2

RESULT 30
 E06917/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 E06917, cDNA positive strand virus, no DNA state, Flaviviridae;
 Hepatitis C virus.
 REFERENCE
 1 (bases 1 to 23)
 Okamoto, H. and Nakamura, T.
 METHOD FOR DETECTING DIVERSITY OF HCV GENOM AND PRIMER THEREIN
 JOURNAL
 IMMO JAPAN:KK
 COMMENT
 OS Hepatitis C virus
 PN CP 1994/0800-A/6
 PD 15-MAR-1994
 PE 26-APR-1994 OF 19920054
 FI OKAMOTO HIRAKAWA, NAKAMURA TETSUO
 1..23
 /organism="Hepatitis C virus"
 /db_xref="taxon:3606"
 FEATURES
 SOURCE
 1..23
 /organism="Hepatitis C virus"
 /db_xref="taxon:3606"
 BASE COUNT 7 a 6 c 7 g 3 t
 ORIGIN
 Query Match 43 74; Score 13; E=6; Length 23;
 Best local similarity 26.0; First No. 3,990,057
 Matches 15; Conservation 0; Mismatches 5; Indels 0; Gaps 0
 CY 6 TCGGCGCGGCGTGAATCTTC 26
 DB 23 TCGGCGCGGCGTGAATCTTC 3
 RESULT 31
 AX249699
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Carnivora; Varigata; Eumetazoa;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 31)
 Bergsma, D.J. and Tanigawa, M.
 Ligands of the hepatotropic protein HPGAN2
 Patent: US 6001674 A 14-07-1999.
 FEATURES
 SOURCE
 1..31
 /organism="Homo sapiens"
 /db_xref="taxon:3606"
 BASE COUNT 11 a 3 c 6 g 10 t 1 others
 ORIGIN
 Query Match 43 74; Score 13; E=6; Length 31;
 Best local similarity 26.0; First No. 3,990,057

[illegible]

AP122853	LOCUS	Sequence 75 from patent US 6168778	Linear	FAT 16 MAY 2001
DEFINITION	AP122853			
ACCESSION	AP122853			
VERSION	AP122853.1	GI:14197813		
KEYWORDS				
SOURCE	Unknown			
ORGANISM	Unknown			
REFERENCE	1. (Pages 1 to 29)			
AUTHORS	Jancic N., Gold, L., Schmidt, P. and Vargese, C.			
TITLE	Vascular endothelial growth factor (VEGF) Neutral Acid ligand			
GENERAL	Complexes			
FEATURES	Parent: US 6168778 A 75: 92 CAN 2001.			
SOURCE	Location/Qualifiers			
	1..29			
BASE COUNT	9 a 4 c 12 g 4 t			
ORIGIN				
Query Match	46.0% Score 13.4 (E 6)	Length 29		
Best Local Similarity	88.2% Prod No 1 to 0			
Matches	15 Consecutive 0 Mismatches 2 Indels 0 Gaps 0			
QY	6 TGGGTAAAGAGATG 22			
Db	6 TGGGTAAAGAGATG 22			
RESULT 17	AP122854	49 bp	Linear	FAT 16 MAY 2001
LOCUS	AP122854			
DEFINITION	Sequence 76 from patent US 6168778			
ACCESSION	AP122854			
VERSION	AP122854.1	GI:14197820		
KEYWORDS				
SOURCE	Unknown			
ORGANISM	Unknown			
REFERENCE	Unclassified			
AUTHORS	Jancic N., Gold, L., Schmidt, P. and Vargese, C.			
TITLE	Vascular endothelial growth factor (VEGF) Neutral Acid ligand			
GENERAL	Complexes			
FEATURES	Parent: US 6168778 A 76: 92 CAN 2001.			
SOURCE	Location/Qualifiers			
	1..29			
BASE COUNT	9 a 4 c 12 g 4 t			
ORIGIN				
Query Match	46.0% Score 13.4 (E 6)	Length 29		
Best Local Similarity	88.2% Prod No 1 to 0			
Matches	15 Consecutive 0 Mismatches 2 Indels 0 Gaps 0			
QY	6 TGGGTAAAGAGATG 22			
Db	6 TGGGTAAAGAGATG 22			
RESULT 18	AP122855	59 bp	Linear	FAT 16 MAY 2001
LOCUS	AP122855			
DEFINITION	Sequence 77 from patent US 6168778			
ACCESSION	AP122855			
VERSION	AP122855.1	GI:14197821		
KEYWORDS				
SOURCE	Unknown			
ORGANISM	Unknown			
REFERENCE	Unclassified			
AUTHORS	Jancic N., Gold, L., Schmidt, P. and Vargese, C.			
TITLE	Vascular endothelial growth factor (VEGF) Neutral Acid ligand			

JOURNAL	Patient: US 6168778-A 77 02 JAN 2001
FEATURES	1: 41 0/Qualifiers
SOURCE	1: 29
ORGANISM	/organism="unknown"
BASE COUNT	3 4 4 12 9 4 1
ORIGIN	
Query Match	46.0% Score 13.8; PB 6; Length 207
Best Local Similarity	AP 28; Prod No. 1.7e+05
Matches	15; Conservative 0; Mismatch 2; Indels 1; Gaps 2
1	6 TTTCTATATATATG 22
2	
3	6 TGTATATATATG 22
4	
5	6 TGTATATATATG 22
6	
7	6 TTTCTATATATG 22
8	
9	6 TTTCTATATATG 22
10	
11	6 TTTCTATATATG 22
12	
13	6 TTTCTATATATG 22
14	
15	6 TTTCTATATATG 22
16	
17	6 TTTCTATATATG 22
18	
19	6 TTTCTATATATG 22
20	
21	6 TTTCTATATATG 22
22	
23	6 TTTCTATATATG 22
24	
25	6 TTTCTATATATG 22
26	
27	6 TTTCTATATATG 22
28	
29	6 TTTCTATATATG 22
30	
31	6 TTTCTATATATG 22
32	
33	6 TTTCTATATATG 22
34	
35	6 TTTCTATATATG 22
36	
37	6 TTTCTATATATG 22
38	
39	6 TTTCTATATATG 22
40	
41	6 TTTCTATATATG 22
42	
43	6 TTTCTATATATG 22
44	
45	6 TTTCTATATATG 22
46	
47	6 TTTCTATATATG 22
48	
49	6 TTTCTATATATG 22
50	
51	6 TTTCTATATATG 22
52	
53	6 TTTCTATATATG 22
54	
55	6 TTTCTATATATG 22
56	
57	6 TTTCTATATATG 22
58	
59	6 TTTCTATATATG 22
60	
61	6 TTTCTATATATG 22
62	
63	6 TTTCTATATATG 22
64	
65	6 TTTCTATATATG 22
66	
67	6 TTTCTATATATG 22
68	
69	6 TTTCTATATATG 22
70	
71	6 TTTCTATATATG 22
72	
73	6 TTTCTATATATG 22
74	
75	6 TTTCTATATATG 22
76	
77	6 TTTCTATATATG 22
78	
79	6 TTTCTATATATG 22
80	
81	6 TTTCTATATATG 22
82	
83	6 TTTCTATATATG 22
84	
85	6 TTTCTATATATG 22
86	
87	6 TTTCTATATATG 22
88	
89	6 TTTCTATATATG 22
90	
91	6 TTTCTATATATG 22
92	
93	6 TTTCTATATATG 22
94	
95	6 TTTCTATATATG 22
96	
97	6 TTTCTATATATG 22
98	
99	6 TTTCTATATATG 22
100	

ORIGIN

Query Match 47.3% Score 14.21 DB 6 Length 307
 Best Local Similarity 70.4% Prod. No. 1.7e-05
 Matches 15 Conservative 0 Mismatches 5 Indels 0 Gaps 0

CY 3 AATTGGCGAAGAGATTGTTCTGT 29
 |||||
 3 AATTGGCGAAGAGATTGTTCTGT 29

DB 3 AATTGGCGAAGAGATTGTTCTGT 29

RESULT 12
 E3.961/c
 LOCUS
 DEFINITION Novel cancer metastasis marker
 ACCESSION E3961
 VERSION E3961.1 GI:1071400
 KEYWORDS
 SOURCE unclassified
 ORGANISM unclassified

REFERENCE 1 (bases 1 to 22)
 Masamitsu T, Mami S, Fujisueguchi H, and Ikemochi Y
 Authors Novel cancer metastasis marker
 Journal Patent: JP 199911991 A 15 16 Nov 1999
 TAF99A EMP20 00 LTP
 CC Unclassified
 PN JP 199911991 A/15
 PD 16-NOV-1999
 RF CI MAY 1999 JP 1999-11991

FEATURES
 source
 location/Qualifiers
 1..22 /organism="unclassified"
 /db_xref="taxon:32644"

BASE COUNT
 ORIGIN
 6 a 6 c 5 g 5 t

Query Match 46.0% Score 13.81 DB 6 Length 29
 Best Local Similarity 70.4% Prod. No. 1.7e-05
 Matches 15 Conservative 0 Mismatches 5 Indels 0 Gaps 0

CY 6 TGCGGCAAGAGATTGTTCT 27
 |||||
 22 TGCGGCAAGAGATTGTTCT 1

DB 22 TGCGGCAAGAGATTGTTCT 1

RESULT 13
 AR122834
 LOCUS
 DEFINITION Sequence 56 from patent US 6168778
 ACCESSION AR122834
 VERSION AR122834.1 GI:1107800
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 unclassified
 1 (bases 1 to 29)
 Janjic N, Gold L, Schmidt P, and Vargese C
 Authors Vascular endothelial growth factor (VEGF) Nucleic Acid Library
 Title Complexes
 Journal Patent: US 6168778 A 06 02 JAN 2001
 Features Location/Qualifiers
 1..28 /organism="unknown"

BASE COUNT
 ORIGIN
 9 a 3 c 12 g 4 t

BASE COUNT 9 a 3 c 12 g 4 t

ORIGIN

Query Match 46.0% Score 13.81 DB 6 Length 29
 Best Local Similarity 70.4% Prod. No. 1.7e-05
 Matches 15 Conservative 0 Mismatches 5 Indels 0 Gaps 0

CY 6 TGCGGCAAGAGATTGTTCT 27
 |||||
 22 TGCGGCAAGAGATTGTTCT 1

DB 22 TGCGGCAAGAGATTGTTCT 1

RESULT 14
 AR122845
 LOCUS
 DEFINITION Sequence 57 from patent US 6168778
 ACCESSION AR122845
 VERSION AR122845.1 GI:14107801
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 unclassified
 1 (bases 1 to 28)
 Janjic N, Gold L, Schmidt P, and Vargese C
 Authors Vascular endothelial growth factor (VEGF) Nucleic Acid Library
 Title Complexes
 Journal Patent: US 6168778 A 06 02 JAN 2001
 Features Location/Qualifiers
 1..28 /organism="unknown"

BASE COUNT
 ORIGIN
 9 a 4 c 11 g 4 t

Query Match 46.0% Score 13.81 DB 6 Length 29
 Best Local Similarity 70.4% Prod. No. 1.7e-05
 Matches 15 Conservative 0 Mismatches 5 Indels 0 Gaps 0

CY 6 TGCGGCAAGAGATTGTTCT 27
 |||||
 22 TGCGGCAAGAGATTGTTCT 1

DB 22 TGCGGCAAGAGATTGTTCT 1

RESULT 15
 AR122852
 LOCUS
 DEFINITION Sequence 58 from patent US 6168778
 ACCESSION AR122852
 VERSION AR122852.1 GI:14107818
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 unclassified
 1 (bases 1 to 29)
 Janjic N, Gold L, Schmidt P, and Vargese C
 Authors Vascular endothelial growth factor (VEGF) Nucleic Acid Library
 Title Complexes
 Journal Patent: US 6168778 A 06 02 JAN 2001
 Features Location/Qualifiers
 1..29 /organism="unknown"

BASE COUNT
 ORIGIN
 9 a 4 c 12 g 4 t

FEATURES

source

Location/Qualifiers

BASE COUNT 10 a 10 c 4 g 6 t

Query Match 59.3% Score 26.8, E 6, Length 30;
Best Local Similarity 92.3% Prod No: 0.06;
Matches 28, Conservative 0, Mismatches 2, Indels 0, Gaps 0;

Db 1 GATATTGCTTAAAGAGAAATGTTCTGTC 30
1 GATATTGCTTAAAGAGAAATGTTCTGTC 1

RESULT 4

AX02893

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

ORIGIN

BASE COUNT

ORIGIN

FEATURES

source

Location/Qualifiers

Query Match 59.3% Score 26.8, E 6, Length 30;
Best Local Similarity 92.3% Prod No: 0.06;
Matches 28, Conservative 0, Mismatches 2, Indels 0, Gaps 0;

Db 1 GATATTGCTTAAAGAGAAATGTTCTGTC 30
1 GATATTGCTTAAAGAGAAATGTTCTGTC 1

RESULT 5
AX02893
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
ORIGIN

BASE COUNT 10 a 10 c 4 g 6 t

Query Match 59.3% Score 26.8, E 6, Length 30;
Best Local Similarity 92.3% Prod No: 0.06;
Matches 28, Conservative 0, Mismatches 2, Indels 0, Gaps 0;

Db 1 GATATTGCTTAAAGAGAAATGTTCTGTC 30
1 GATATTGCTTAAAGAGAAATGTTCTGTC 1

RESULT 6
AX128301
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
ORIGIN

BASE COUNT 10 a 10 c 4 g 6 t

Query Match 57.3% Score 17.2, E 6, Length 30;
Best Local Similarity 78.3% Prod No: 0.03;
Matches 28, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

Db 1 GATATTGCTTAAAGAGAAATGTTCTGTC 30
1 GATATTGCTTAAAGAGAAATGTTCTGTC 30

RESULT 6
AX128301
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
ORIGIN

BASE COUNT 10 a 10 c 4 g 6 t

Query Match 57.3% Score 17.2, E 6, Length 30;
Best Local Similarity 78.3% Prod No: 0.03;
Matches 28, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

Db 1 GATATTGCTTAAAGAGAAATGTTCTGTC 30
1 GATATTGCTTAAAGAGAAATGTTCTGTC 30

RESULT 7
E16238
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
ORIGIN

BASE COUNT 10 a 10 c 4 g 6 t

Query Match 49.3% Score 14.8, E 6, Length 30;
Best Local Similarity 78.3% Prod No: 0.03;
Matches 28, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

Db 1 GATATTGCTTAAAGAGAAATGTTCTGTC 30
1 GATATTGCTTAAAGAGAAATGTTCTGTC 30

RESULT 8
E16238
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
ORIGIN

BASE COUNT 10 a 10 c 4 g 6 t

Query Match 49.3% Score 14.8, E 6, Length 30;
Best Local Similarity 78.3% Prod No: 0.03;
Matches 28, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

Db 1 GATATTGCTTAAAGAGAAATGTTCTGTC 30
1 GATATTGCTTAAAGAGAAATGTTCTGTC 30

RESULT 9
E16238
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
ORIGIN

BASE COUNT 10 a 10 c 4 g 6 t

Query Match 49.3% Score 14.8, E 6, Length 30;
Best Local Similarity 78.3% Prod No: 0.03;
Matches 28, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

Db 1 GATATTGCTTAAAGAGAAATGTTCTGTC 30
1 GATATTGCTTAAAGAGAAATGTTCTGTC 30

RESULT 10
E16238
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
ORIGIN

BASE COUNT 10 a 10 c 4 g 6 t

[illegible]

